

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:52:10 ; Search time 22 Seconds  
(without alignments)  
529.192 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642

Sequence: 1 MSQFRVSPLDRTWNLGETVE.....IMYFSHFVFLPAKPTTTP 121

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	99.2	235	1	RWHUT8 T-cell surface gly
2	599	93.3	198	2	S25656 T-cell surface gly
3	366.5	57.1	239	2	I46082 CD8 alpha-chain -
4	347.5	54.1	242	2	S25663 T-cell surface gly
5	248	38.6	236	2	A24637 T-cell surface gly
6	239	37.2	247	1	RWMST2 T-cell surface gly
7	238	37.1	220	2	I55963 T-cell surface gly
8	238	37.1	247	2	A34954 T-cell surface gly
9	227.5	35.4	246	2	A29523 T-cell surface gly
10	155	24.1	235	2	I50610 T-cell surface gly
11	130.5	20.3	230	2	S49449 T-cell surface gly
12	122.5	19.1	213	2	A21177 T-cell surface gly
13	121.5	18.9	106	2	S38495 T-cell surface gly
14	120.5	18.8	107	2	PLU080 T-cell surface gly
15	119.5	18.6	107	2	B46516 T-cell surface gly
16	119	18.5	99	2	S36058 T-cell surface gly
17	117.5	18.3	113	1	L1CHV T-cell surface gly
18	117.5	18.3	125	2	A31493 T-cell surface gly
19	116.5	18.1	233	2	S25744 T-cell surface gly
20	116	18.1	231	2	S25753 T-cell surface gly
21	114	17.8	151	2	S24064 T-cell surface gly
22	113	17.6	146	2	S02083 T-cell surface gly
23	111.5	17.4	108	1	KVMS06 T-cell surface gly
24	111	17.3	112	2	S46395 T-cell surface gly
25	111	17.3	112	2	S09970 T-cell surface gly
26	111	17.3	219	2	S38865 T-cell surface gly
27	110.5	17.2	107	2	S12954 T-cell surface gly
28	110.5	17.2	114	2	S40375 T-cell surface gly
29	110.5	17.2	235	2	S25758 T-cell surface gly

30	110	17.1	99	2	S36056 Ig lambda chain -
31	110	17.1	112	2	S58207 Ig light chain V r
32	110	17.1	132	2	S26882 Ig kappa chain V r
33	110	17.1	135	2	S40342 Ig kappa chain - h
34	110	17.1	136	2	S40357 Ig kappa chain V-J
35	110	17.1	231	2	S25751 Ig lambda chain -
36	109.5	17.1	97	2	I51216 Ig light chain var
37	109.5	17.1	98	2	PH1069 Ig light chain V r
38	109.5	17.1	106	2	B47329 Ig kappa chain V r
39	109.5	17.1	111	2	S36281 Ig lambda chain V
40	109.5	17.1	112	2	S58206 Ig light chain V r
41	109.5	17.1	113	1	KVMS26 Ig kappa chain V r
42	109.5	17.1	128	2	S31488 Ig kappa chain pre
43	109.5	17.1	132	2	PH0106 anti-digoxin trans
44	109.5	17.1	233	2	S25741 Ig lambda chain -
45	109	17.0	110	1	L2HU58 Ig lambda chain V-

ALIGNMENTS

RESULT 1  
RWHUT8  
T-cell surface glycoprotein CD8 alpha chain precursor - human  
N/Alternate names: Leu-2/T8 T lymphocyte differentiation antigen; T-cell surface antigen  
N/Contains: T-cell surface glycoprotein CD8 alpha chain secreted splice form; T-cell su  
C/Species: Homo sapiens (man)  
C/Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004  
C/Accession: A30604; A45888; A01999; A22824; A90096; A31458; B31458; JP0105  
R/Normant, A.M.; Lonberg, N.; Lacy, E.; Littman, D.R.  
J. Immunol. 142, 3312-3319, 1989  
A/Title: Alternatively spliced mRNA encodes a secreted form of human CD8-alpha. Charact  
A/Reference number: A30604; MUID:89215302; PMID:2496167  
A/Accession: A30604  
A/Molecule type: DNA  
A/Residues: 1-235 <NOR>  
A/Cross-references: UNIPROT:P01732; UNIPARC:UPI00001273B4; GB:M26315; NID:g341466; PIDN  
R/Nakayama, K.; Tokito, S.; Okumura, K.; Nakachi, H.  
Immunogenetics 30, 393-397, 1989  
A/Title: Structure and expression of the gene encoding CD8-alpha chain (Leu-2/T8).  
A/Reference number: A45888; MUID:90035142; PMID:2509342  
A/Accession: A45888  
A/Molecule type: DNA  
A/Residues: 1-235 <NAK>  
A/Cross-references: UNIPARC:UPI00001273B4; GB:M27161; NID:g187844; PIDN:AAA59674.1; PID  
A/Note: the authors translated the codon TCG for residue 116 as Cys and GCC for residue  
R/Littman, D.R.; Thomas, Y.; Maddon, P.J.; Chess, L.; Axel, R.  
Cell 40, 237-246, 1985  
A/Title: The isolation and sequence of the gene encoding T8: a molecule defining functi.  
A/Reference number: A01999; MUID:85099337; PMID:3871356  
A/Accession: A01999  
A/Molecule type: mRNA  
A/Residues: 1-235 <LIT>  
A/Cross-references: UNIPARC:UPI00001273B4; GB:M12828; NID:g179145; PIDN:AAB04637.1; PID  
A/Experimental source: clones pT8.B and pT8.F1  
R/Sukhatme, V.P.; Sizer, K.C.; Volmer, A.C.; Hunkapiller, T.; Parnes, J.R.  
Cell 40, 591-597, 1985  
A/Title: The T cell differentiation antigen Leu-2/T8 is homologous to immunoglobulin an  
A/Reference number: A22824; MUID:85124610; PMID:3918796  
A/Accession: A22824  
A/Molecule type: mRNA  
A/Residues: 1-235 <SUK>  
A/Cross-references: UNIPARC:UPI00001273B4; GB:M12824; NID:g339426; PIDN:AAA61133.1; PID  
R/Parnes, J.R.; Sizer, K.C.; Sukhatme, V.P.; Hunkapiller, T.  
Behring Inst. Mitt. 77, 48-55, 1985  
A/Title: Structure of Leu-2/T8 as deduced from the sequence of a cDNA clone.  
A/Reference number: A90096; MUID:86103103; PMID:3936473  
A/Accession: A90096  
A/Molecule type: mRNA  
A/Residues: 1-235 <PAR>  
A/Cross-references: UNIPARC:UPI00001273B4  
R/Giblin, P.; Ledbetter, J.A.; Kavathas, P.  
Proc. Natl. Acad. Sci. U.S.A. 86, 998-1002, 1989

```

A/Title: A secreted form of the human lymphocyte cell surface molecule CD8 arises from
A/Reference number: A31458; MUID:89128905; PMID:2536941
A/Accession: A31458
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 168-235 <GIB>
A/Cross-references: UNIPARC:UPI0000173727
A/Note: this mRNA fragment represents the transmembrane form
A/Accession: B31458
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 168-171,'G',210-235 <G12>
A/Cross-references: UNIPARC:UPI0000173728
A/Note: this mRNA fragment represents the secreted form
A/Note: the cited Genbank accession number, J04165, is not in release
R/Snow, P.M.; Terhorst, C.
J. Biol. Chem. 258, 14675-14681, 1983
A/Reference number: A92407; MUID:84061928; PMID:6605969
A/Contents: annotation
C/Comment: This protein was shown in reference A92407 to be in a multimeric complex of
C/Comment: Alternative splicing leads to the production of a secreted form lacking the
C/Genetics:
A/Gene: GDB:CD8A
A/Cross-references: GDB:120581; OMIM:186910
A/Map position: 2p12-2p12
A/Intons: 17/1; 135/1; 172/1, 209/1; 219/2
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: alternative splicing; extracellular protein; glycoprotein; heterotetramer;
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-235/Product: T-cell surface glycoprotein CD8 alpha chain transmembrane splice form
F/22-171,209-235/Product: T-cell surface glycoprotein CD8 alpha chain secreted splice fo
F/36-117/Domain: immunoglobulin homology <IMM>
F/118-182/Domain: hinge <HNG>
F/183-205/Domain: transmembrane #status predicted <TMB>
F/206-235/Domain: intracellular #status predicted <INT>
F/43-115/Disulfide bonds: #status predicted
F/49/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/181/Disulfide bonds: interchain #status predicted

Query Match          99.2%; Score 637; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  SQFRVSPDLRTWNLGETVEELKQVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
      |||
Db      22  SQFRVSPDLRTWNLGETVEELKQVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 81

QY      62  EGLDQRFSGSKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPVFLPAKPTTP 121
      |||
Db      82  EGLDQRFSGSKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPVFLPAKPTTP 141

RESULT 2
S25656
T-cell surface glycoprotein CD8 alpha chain precursor - orangutan
C/Species: Pongo pygmaeus (orangutan)
C/Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
C/Accession: S25656
R/Lawlor, D.A.; Parham, P.
Immunogenetics 36, 121-125, 1992
A/Title: Structure of CD8 alpha and beta chains of the orangutan: novel patterns of mRNA
A/Reference number: S25656; MUID:92307742; PMID:1612644
A/Accession: S25656
A/Molecule type: mRNA
A/Residues: 1-198 <LAW>
A/Cross-references: UNIPROT:P30433; UNIPARC:UPI00001273B5; EMBL:X60223; NID:g38144; PIDN
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: alternative splicing; extracellular protein; glycoprotein; heterotetramer;
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-198/Product: T-cell surface glycoprotein CD8 alpha chain #status predicted <MAT>
F/36-117/Domain: immunoglobulin homology <IMM>
F/146-168/Domain: transmembrane #status predicted <TMB>
F/169-198/Domain: intracellular #status predicted <INT>

```

```
F;43-115/Disulfide bonds: #status predicted
F;49/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;144/Disulfide bonds: interchain #status predicted
```

Query Match	93.3%;	Score 599;	DB 2;	Length 198;
Best Local Similarity	100.0%;	Pred. No. 1.4e-52;		
Matches 113; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

### RESULT 3

CD8 alpha-chain - cat  
C/Species: Felis silvestris catus (domestic cat)  
C/Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I46082  
R/Pecoraro, M.; Kawaguchi, Y.; Miyazawa, T.; Norimine, J.; Maeda, K.; Toyosaki, T.; Tohyama, H.  
Immunology 81, 127-131, 1994  
A/Title: Isolation, sequence and expression of a cDNA encoding the alpha-chain of the feline CD8 antigen  
A/Reference number: I46082; MUID:94178799; PMID:8132208  
A/Accession: I46082  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-239 <PEC>  
A/Cross-references: UNIPROT:P41688; UNIPARC:UPI00001273B3; GB:D16536; NID:g485385; PIDN:PI000000000  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match	57.1%;	Score 366.5;	DB 2;	Length 239;
Best Local Similarity	58.7%;	Pred. No. 3e-29;		
Matches 71; Conservative	19;	Mismatches 30;	Indels 1;	Gaps 1;

[illegible]

QY	121	P	121
DB	145	P	145

## RESULT 4

T-cell surface glycoprotein CD8 alpha chain - bovine  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: S25663  
 R/Lalor, P.; Buccì, C.; Fornaro, M.; Rattazzi, M.C.; Nakauchi, H.; Herzenberg, L.A.; Al  
 Immunology 76, 95-102, 1992  
 A/Title: Molecular cloning, reconstruction and expression of the gene encoding the alph  
 A/Reference number: S25663; MVID:92332098; PMID:1628904  
 A/Accession: S25663  
 A/Status: Preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-242 <LAL>  
 A/Cross-references: UNIPROT:P31783; UNIPARC:UPI00001273B1; EMBL:X59416; NID:g190; PIDN:  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: glycoprotein; transmembrane protein

Query Match	54.1%;	Score 347.5;	DB 2;	Length 242;
Best Local Similarity	57.1%;	Pred. No. 2.4e-27;		
Matches 68;	Conservative 17;	Mismatches 33;	Indels 1;	Gaps 1;

QY 4 PRVSPLDRTWNLGETVEYLKCQVLLSNPTSGSCMWLFQPRGAAASPTELLYLQNKPKAAEG 63

Db 28 FRMSPTQKETRLGEXVELQCELLQSGMATGCSWLRIHPGDDPRPTFLMYLSAQRYKLAEG 87

QY 64 LDTQRFSGKRL-GDTFVLLTSLDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121

Db 88 LDPRHISGAKVSGTYKFQULTLSSFLQEDQGYFCSVVSNSILYFSNFVFPVFLPAKPAATTTP 146

## RESULT 5

T-cell surface glycoprotein CD8 alpha chain precursor - rat  
N:Alternate names: MRC OX-8 antigen  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Sep-1987 #sequence\_revision 17-Sep-1987 #text\_change 09-Jul-2004  
C:Accession: A24637  
R:Johnson, P.; Gagnon, J.; Barclay, A.N.; Williams, A.F.  
EMBO J. 4, 2539-2545, 1985  
A:Title: Purification, chain separation and sequence of the MRC OX-8 antigen, a marker  
A:Reference number: A24637; MUID:86030231; PMID:3932064  
A:Accession: A24637  
A:Molecule type: mRNA  
A:Residues: 1-236 <JOH>  
A:Cross-references: UNIPROT:P07725, UNIPARC:UPI00001273B6; GB:X03015; NID:g55720; PIDN:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; heterodimer; surface antigen; transmembrane protein  
F:40-121/Domain: immunoglobulin homology <IMM>

**Query Match**

Query Match	38.6%;	Score 248;	DB 2;	Length 236;
Best Local Similarity	41.4%;	Pred. No. 2e-17;		
Matches	53;	Conservative	25;	Mismatches 40;
				Indels 10;
				Gaps 4;

[illegible]

## RESULT 6

T-cell surface glycoprotein CD8 alpha chain precursor - mouse  
N/A  
Alternate names: T-cell surface antigen Lyt-2

C/Date: 28-May1986 #sequence revision 28-May-1986 #text\_change 09-Jul-2004  
C/Accession: A01998; A24784; I71903  
R/Nakauchi, H.; Nolan, G.P.; Hsu, C.; Huang, H.S.; Kavathas, P.; Herzenberg, L.A.  
proc. Natl. Acad. Sci. U.S.A. 82, 5126-5130, 1985  
A/Title: Molecular cloning of Iyt-2, a membrane glycoprotein marking a subset of mouse T  
A/Reference number: A01998; MUID:85270477; PMID:3927298  
A/Accession: A01998

A;Molecule type: mRNA  
A;Residues: 1-247 <NAK>  
A;Cross-references: UNIPROT:P01731; UNIPARC:UPI00000270C4; GB:M12825; GB:M16980; NID:g19  
A;Experimental source: strain BALB/c  
A;Zamoyaska, R.; Vollmer, A.C.; Sizer, K.C.; Liaw, C.W.; Parnes, J.R.  
Cell 43, 153-163, 1985  
A;Title: Two Lys-2 polypeptides arise from a single gene by alternative splicing pattern  
A;Reference number: A24784; MUID:86079485; PMID:3935316

A/Accession: A24784  
A/Molecule type: mRNA  
A/Residues: 1-247 <ZAM>  
A/Cross-references: UNIPARC:UPI00000270C4; GB:M12052; NID:G198973; PIDN:AAA39478.1; PID:R1Law, C.W.; Zamoyaska, R.; Parnes, J.R.  
J. Immunol. 137, 1037-1043, 1986  
A/Title: Structure, sequence, and polymorphism of the Lyt-2 T cell differentiation antigen  
A/Reference number: I55963; MUID:86252252; PMID:3487583

A;Accession: I71903  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-247 <RES>  
A;Cross-references: UNIPARC:UPI00000270C4; GB:MI2977; NID:g198966; PIDN:AAA39475.1; PID  
A;Note: allelic form Lyt-2.2  
C;Comment: The glycoprotein Lyt-2 is the mouse homolog of the human T8 molecule.

A; Introns: 149/1; 184/1; 221/1; 231/2  
C; Superfamily: immunoglobulin V region; immunoglobulin homology  
C; Keywords: alternative splicing; glycoprotein; heterodimer; heterotrimer; T-cell; tr  
F; 1-27/Domain: signal sequence #status predicted <SIG>  
F; 28-247/Product: T-cell surface glycoprotein CD8 #status predicted <MAT>  
F; 46-131/Domain: immunoglobulin homology <IMM>  
F; 140-183/Domain: extracellular spacer #status predicted <EXT>  
F; 184-220/Domain: transmembrane #status predicted <TM>  
F; 221-247/Domain: intracellular #status predicted <INT>  
F; 53-129/Disulfide bonds: #status predicted  
F; 69, 97, 150/Binding site: carbohydrate (Asn) (covalent) #status predicted

**Query Match**

Query Match	37.2%;	Score 239;	DB 1;	Length 247;
Best Local Similarity	44.7%;	Pred. No. 1.7e-16;		
Matches	55;	Conservative	20;	Mismatches 42;
				Indels 6;
				Gaps 5;

```

Oy      3 QFRVSPDLRTWNLGETVELKCQVLLSNPTSGCSWLQPRGA--AASPTFLYL--SQNKPK 59
      : : | | : | : | : : | | | | | : | | | | : | |
Db      33 ELRIPPKMDAELGQKVDLVCEV-LGSVSGCSWLQFONSSSKLPQPTFVVYMASSHNKIT 91

```

Qy 60 AAEGLDTPF-FSGKR-LGDTFVLTLSDFERRNEGYYFCALSNSIMYFSHFVPVFLPAKP 117  
|:::||:||||||:|||||||  
Db 92 WDEKLNSSKLFSAMRDITNNKYVLTLNFKSKENEGYYPFCSVTSNSVMYFFSSVVPVLÖKVNS 151

QY	118	TTT	120
Db	152	TTTT	154

## RESULT 7

Lyt-2.1 lymphocyte differentiation antigen - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I55963  
R/Liaw, C.W.; Zamoycka, R.; Parnes, J.R.  
J. Immunol. 137, 1037-1043, 1986  
A/Title: Structure, sequence, and polymorphism of the Lyt-2 T cell differentiation anti-  
A/Reference number: I55963; MUID:86252252; PMID:3487583  
A/Accession: I55963  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-220 <RES>  
A/Cross-references: UNIPROT:Q61816; UNIPARC:UPI00000E7DDE; GB:M12979; NID:g198960; PIDN:  
C/Genetics:  
A/Introns: 149/1, 184/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F/46-131/Domain: immunoglobulin homology <IMM>

**Query Match**

Query Match	37.1%;	Score 238;	DB 2;	Length 220;
Best Local Similarity	44.7%;	Pred. No. 1.9e-16;		
Matches	55;	Conservative	20;	Mismatches 42;
				Indels 6;
				Gaps 5;

```
Oy      3 QFRVSPILDRITNLGETVELKCOQVLNPTSGCWLFOPRGA--AASPTFLLYL--SQNKPK   59  
          :|::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db     33 ELRLTFPPKKMDALGQKVLDYCEV-LGSVSQGCSWLPFONSSSKLPQTFFVVVMASSINKIT  91
```

```

Qy 60 AAEGLDQÖR-FSGKR-LGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHPVPVFLPAKP 117
    |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 92 WDEKLNSSKLPFAVRDITNNKYTLTNKFSKENEGYFCSVYSNSVMYFSSVVPVLÖKUNS 151

```

QY	118	TTT	120
Db	152	TTT	154

```

RESULT 8
A34954
T-cell surface glycoprotein Lyt-2 precursor (strain C.AKR) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Sep-1990 #sequence_revision 03-Jun-1993 #text_change 21-Jan-2000
C/Accession: A34954
R/Youn, H.J.; Harris, J.V.; Gottlieb, P.D.
Immunogenetics 28, 345-352, 1988
A/Title: Nucleotide sequence analysis of the C.AKR Lyt-2(a) gene: structural polymorphisms
A/Reference number: A34954; MUID:89006895; PMID:3267233
A/Accession: A34954
A/Molecule type: DNA
A/Residues: 1-247 <YOU>
A/Cross-references: UNIPARC:UPI000016CEFF; GB:M22064; NID:g199569; PIDN:AAA39665.1; PID:
A/Note: the authors translated the codon CCT for residue 208 as Leu
C/Genetics:
A/Introns: 149/1; 184/1; 221/1; 231/2
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: glycoprotein; transmembrane protein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-247/Product: T-cell surface glycoprotein Lyt-2 #status predicted <MAT>
F;46-131/Domain: immunoglobulin homology <IMM>

```

[illegible]

RESULT 9  
A29523  
T-cell surface glycoprotein Lyt-2 precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A29523  
R/Nakauchi, H.; Tagawa, M.; Nolan, G.P.; Herzenberg, L.A.  
Nucleic Acids Res. 15, 4337-4347, 1987  
A/Title: Isolation and characterization of the gene for the murine T cell differentiation  
A/Reference number: A29523; MUID:87231009; PMID:3495785  
A/Accession: A29523  
A/Molecule type: DNA  
A/Residues: 1-246 <NAK>  
A/Cross-references: UNIPROT:P01731; UNIPARC:UPI000016CEC2; GB:Y00157; NID:g52967; PIDN:C  
C/Genetics:  
A/Introns: 148/1; 183/1; 220/1; 230/2  
C/Superfamily: immunoglobulin V region, immunoglobulin homology  
C/Keywords: glycoprotein; transmembrane protein  
F/46-130/Domain: immunoglobulin homology <IMM>

	Query Match	35.4%;	Score 227.5;	DB 2;	length 246;
	Best Local Similarity	44.3%;	Pred. No.2.4e-15;		
	Matches	54;	Conservative 19;	Mismatches 44;	Indels 5; Gaps 5;
OY	3 QFRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFPQPRGA-AASPTFL-LYLSQNKPKA	60	:	:	:
Dd	33 ELRIFFPKGMDAELGQKVLDVCEV-LGSVSQGCSMLFQNSSSKLPQPFTFYVMASHHNKITW	91	:	:	:
OY	61 AEGLDTOR-FSGKR-LGDTFVLTUSDFFRENENGYIFCSALSNSIMYFSHFVPVFLLPAKPT	118	:	:	:
Dd	92 DEKLNSSKLFSAMRDTNNKYVLTINKFSKENEGYIFCSCVISNSVMYFSSVVPVLQKNST	151	:	:	:

QY	119	TT	120
	152	TT	153

RESULT 10  
I50610  
T-cell surface glycoprotein CD8 alpha chain - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C/Accession: I50610; S33350  
R./Regashes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.U.; Davison, J. Immunol. 154, 4485-4494, 1995  
A./Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha lymphocytes.  
A./Reference number: I50609; MUID:95238946; PMID:7722305  
A./Accession: I50610  
A./Status: preliminary; translated from GB/EMBL/DBJ  
A./Molecule type: mRNA  
A./Residues: 1-235 <TR>  
A./Cross-references: UNIPROT:Q90770; UNIPARC:UPI00000FBABF; EMBL:Z22726; NID:g488149; PIR:G488149  
C./Superfamily: Immunoglobulin V region; immunoglobulin homology  
C./Keywords: glycoprotein

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Query Match          24.1%; Score 155; DB 2; Length 235;
Best Local Similarity 30.7%; Pred. No. 4e-08;
Matches 35; Conservative 24; Mismatches 37; Indels 18; Gaps 4;

QY 16 GETVELKQVLLSNPTSGCSWLFOPRGAASPTFLYLIS-----QNKPKAEGIDTQ 67
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 42 GQRLLECRPF--NSDNGVSWIRQDKDKLH--FIVYISPLSRTTFPQNERTSSQ----- 92

QY 68 RFSGKRLGDTFVULTLSDFRRENEGYYFCSALNSIMYFSHFVPVFLPAKPTTTP 121
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 93 -PEGSKQGGSSFRLLVVKNFKAQDDQGTFFCIANINOMLYFSSGQPAFFPATTTAAP 145

```

```

RESULT 11
S49449
Ig lambda chain - duck
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S49449
R/Magor, R.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
submitted to the EMBL Data Library, October 1994
A/Description: cDNA sequence and organization of the immunoglobulin light chain gene of
A/Reference number: S49449
A/Accession: S49449
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-230 <MAG>
A/Cross-references: UNIPARC:UP100001161F6; EMBL:X82069; NID:9558548; PIDN:CAA57568.1; P
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-106/Domain: immunoglobulin homology <IMM>

```

	Query Match	20.3%	Score 130.5;	DB 2;	Length 230;
	Best Local Similarity	29.5%;	Pred. No. 1.1e-05;		
	Matches	31;	Conservative	21;	Mismatches 38; Indels 15; Gaps 4;
Qy	8 PLDRTNIGETVELKCVLLSNPTSGCSWLFPQPGAAASPFTLLYLSONKPKAEGLDTQ	67			
Dd	26 PASKSVNPGDVTQITC-----SGSSSDYGY-FQQKTGSAFVTVIYQNNKRPSGI----PS	76			
Qy	68 RFSGKRLGDTFVLTLSDFRRENENGYIFCSALNSINSIMWFSHFVPVF	112			
Dd	77 RFGSKSGSTATLTITGVQAEDNAVYYCGS-----YDSSTVGVF	115			

RESULT 12  
A21177  
Ig light chain precursor V-J region - chicken (fragment)  
C,Species: Gallus gallus (chicken)



C/Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 21-Jan-2000  
C/Accession: A21177; B22327  
R;Reynaüd, C.A.; Dahan, A.; Weill, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 80, 4099-4103, 1983  
A/Title: Complete sequence of a chicken lambda light chain immunoglobulin derived from t  
A/Reference number: A21177; MUID:83247424; PMID:6408641  
A/Accession: A21177  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-213 <REY>  
A/Cross-references: UNIPARC:UPI00001148BC; GB:K00678; NID:g212159; PIDN:AAA48906.1; PID:  
R;Reynaüd, C.A.; Anquez, V.; Dahan, A.; Weill, J.C.  
Cell 40, 283-291, 1985  
A/Title: A single rearrangement event generates most of the chicken immunoglobulin light  
A/Reference number: A90861; MUID:85099341; PMID:3917859  
A/Accession: B22327  
A/Molecule type: DNA  
A/Residues: 98-110 <RE2>  
A/Cross-references: UNIPARC:UPI0000176B30  
A/Note: J region  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;20-92/Domain: immunoglobulin homology <IMM>

**This Page Blank (uspto)**







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; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-202
```

```
Query Match      18.6%; Score 119.5; DB 7; Length 98;
Best Local Similarity 34.1%; Pred. No. 6.9e-06;
Matches 31; Conservative 17; Mismatches 32; Indels 11; Gaps 4;
```

```
QY      15 LGETVELKC--QVLLSNPTSGCSWLFQPRGAASPTFLYLSONKPKAAEGLDTORPSG 71
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      14 LRQTATLTCTGNSNIVGN--QGAAMLQOHQG--HPPKLLSYRNNRPSGI----SERFSA 65
```

```
QY      72 KRIGDTFVLTLSDFRRENEGYFCSALSNSI 102
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      66 SRSNGTASLTITGLQPEDEADYCSALDSSL 96
```

RESULT 6  
US-11-136-250-202

```
; Sequence 202, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; PRIOR FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-202
```

```
Query Match      18.6%; Score 119.5; DB 7; Length 98;
Best Local Similarity 34.1%; Pred. No. 6.9e-06;
Matches 31; Conservative 17; Mismatches 32; Indels 11; Gaps 4;
```

```
QY      15 LGETVELKC--QVLLSNPTSGCSWLFQPRGAASPTFLYLSONKPKAAEGLDTORPSG 71
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      14 LRQTATLTCTGNSNIVGN--QGAAMLQOHQG--HPPKLLSYRNNRPSGI----SERFSA 65
```

```
QY      72 KRIGDTFVLTLSDFRRENEGYFCSALSNSI 102
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      66 SRSNGTASLTITGLQPEDEADYCSALDSSL 96
```

RESULT 7  
US-11-084-554-206

```
; Sequence 206, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
```

```
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-206
```

```
Query Match      18.5%; Score 119; DB 7; Length 99;
Best Local Similarity 34.1%; Pred. No. 7.9e-06;
Matches 30; Conservative 15; Mismatches 35; Indels 8; Gaps 3;
```

```
QY      16 GETVELKCQVLLSNPTS--GCSWLFQPRGAASPTFLYLSONKPKAAEGLDTORPSGKR 73
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      15 GQSVTISCTGTSSDVGSYNRVSWYQPPGTA--PKLMIYEVSNRPSGV----PDRFSGSK 68
```

```
QY      74 LGDTFVLTLSDFRRENEGYFCSALSNS 101
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      69 SGN TASLTISGLQAEDEADYCSLYTSS 96
```

RESULT 8  
US-11-136-250-206

```
; Sequence 206, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; PRIOR FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-206
```

```
Query Match      18.5%; Score 119; DB 7; Length 99;
Best Local Similarity 34.1%; Pred. No. 7.9e-06;
Matches 30; Conservative 15; Mismatches 35; Indels 8; Gaps 3;
```

```
QY      16 GETVELKCQVLLSNPTS--GCSWLFQPRGAASPTFLYLSONKPKAAEGLDTORPSGKR 73
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      15 GQSVTISCTGTSSDVGSYNRVSWYQPPGTA--PKLMIYEVSNRPSGV----PDRFSGSK 68
```

```
QY      74 LGDTFVLTLSDFRRENEGYFCSALSNS 101
      |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      69 SGN TASLTISGLQAEDEADYCSLYTSS 96
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RESULT 9  
US-10-952-535A-4

```

; Sequence 4, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-952-535A-4

```

Query Match	18.5%	Score 119;	DB 6;	Length 109;
Best Local Similarity	34.1%;	Pred. No. 8.8e-06;		
Matches	30;	Conservative	16;	Mismatches 34;
			Indels	8;
			Gaps	3;

```

QY      16 GETVELKQVLLSN--PTSGCSWLFQPRGAASPFTLLYLISQNKPKAAEGLDTPQPSGKR 73
      15 GQSTITCTGTSSDIGAVNYVSWYQYPGKA--PKLLTYDVSNRPSGI---SNRPSGSK 68
Db

```

```

QY      74 LGDTFVLTLSDFRRENEGYYECSALSNS 101
      ||| ||| :| :| ||| :| :|
Db      69 SGGDTASTLTISGLQAEDEADYCYCSSFANS 96

```

RESULT 10  
US-10-771

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/ Sequence 64, Application US/10771257
/ Publication No. US20050288864A1
/ GENERAL INFORMATION:
/ APPLICANT: Medical Research Council
/ APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
/ APPLICANT: Cattaneo, Antonino
/ APPLICANT: Maritan, Amos
/ APPLICANT: Visintin, Michela
/ APPLICANT: Rabbitts, Terrence H
/ APPLICANT: Settanni, Giovanni
/ TITLE OF INVENTION: Intracellular antibodies
/ FILE REFERENCE: 18396/2272
/ CURRENT APPLICATION NUMBER: US/10/771,257
/ CURRENT FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: PCT/GB02/03512
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: GB 0119004.0
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: GB 0121577.1
/ PRIOR FILING DATE: 2001-09-06
/ PRIOR APPLICATION NUMBER: GB 0200928.0
/ PRIOR FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: GB 0203569.9
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: IT RM2001A000633
/ PRIOR FILING DATE: 2001-10-25
/ NUMBER OF SEQ ID NOS: 124
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 64
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-771-257-64

```

Query Match	18.5%;	Score 119;	DB 6;	Length 109;
Best Local Similarity	35.9%;	Pred. No. 8.8e-06;		
Matches 33;	Conservative 12;	Mismatches 41;	Indels 6;	Gaps 3;

```

Qy      7 SPLDRWNIGETVEIKCQVLLSNPTSGCSEWLEQPRGAASPTFLTYLSQNKPKAEGLDT 66
      || : : || | : : | : | : | : | : | : | : | : | : | : | : | :
Db      7 SPGTLSLIGERATLSCRASQSVSSSYLANVQCKGQA--PRLLIY--GASRRATGI-P 60

```

QY 67 QRFSGKRLGDTFVLTLTSDFRRENGEYFCSAL 98  
||| | | | : | : | : |  
DB 61 DRFSGSGSCTDFTLTITSSLPEDPFGTYCCQL 92

RESULT 11  
US-11-127-677-62

```

? Sequence 62, Application US/11127677
? Publication No. US20050272107A1
?
? GENERAL INFORMATION:
? APPLICANT: Medical Research Council
? APPLICANT: Rabbits, Terence H
? APPLICANT: Tanaka, Tomoyuki
? TITLE OF INVENTION: Intracellular antibodies
? FILE REFERENCE: 18396/2462
? CURRENT APPLICATION NUMBER: US/11/127,677
? CURRENT FILING DATE: 2005-05-12
? PRIOR APPLICATION NUMBER: PCT/GB03/04942
? PRIOR FILING DATE: 2003-11-14
? PRIOR APPLICATION NUMBER: GB 0226729.2
? PRIOR FILING DATE: 2002-11-15
? NUMBER OF SEQ ID NOS: 150
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 62
? LENGTH: 109
? TYPE: PRT
? ORGANISM: Artificial sequence
? FEATURE:
? OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-62

```

Query Match	18.5%;	Score 119;	DB 7;	Length 109;
Best Local Similarity	35.9%;	Pred. No. 8.8e-06;		
Matches 33;	Conservative 12;	Mismatches 41;	Indels 6;	Gaps 3;

```
QY      7 SPLDRWNIGETVELKCOVLLSNPTSGCSCWLEQPRGAASPTFLLYLSQNKPXAEGLDT   66
        || : ||| | : : : ||| | : ||| : ||| :
Db      7 SPGTLSTLGERATISCRASQSVSSSSYLAWOOKRGOA--PRLIYY--GASRRATGI-P    60
```

QY 67 QRSGLGDTFVLTLSDFRRENGYFCAL 98  
||| | | | : | : | : | : |  
Db 61 DRFSGSGTDFLTLTISLQPEDFGYTCOL 92

## RESULT 12

```

US-10-952-535A-6
; Sequence 6, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:54:16 ; Search time 43 Seconds  
(without alignments)  
1175.752 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642  
Sequence: 1 MSQFRVSPIDRTWNLGETVE.....IMYFSHFVFLPAKPTTTP 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	99.2	198	5	US-10-804-762-3 Sequence 3, Appli
2	637	99.2	198	5	US-10-804-763-3 Sequence 3, Appli
3	637	99.2	218	4	US-10-378-393-20 Sequence 20, Appli
4	637	99.2	219	4	US-10-378-393-3 Sequence 3, Appli
5	637	99.2	219	4	US-10-378-393-13 Sequence 13, Appli
6	637	99.2	235	4	US-10-099-007A-6 Sequence 6, Appli
7	637	99.2	235	4	US-10-207-655-174 Sequence 174, App
8	637	99.2	235	5	US-10-723-860-1244 Sequence 1244, Ap
9	637	99.2	235	5	US-10-804-762-1 Sequence 1, Appli
10	637	99.2	235	5	US-10-804-762-27 Sequence 27, Appli
11	637	99.2	235	5	US-10-804-763-1 Sequence 1, Appli
12	637	99.2	624	4	US-10-378-393-7 Sequence 7, Appli
13	637	99.2	646	4	US-10-378-393-18 Sequence 18, Appli
14	637	99.2	791	4	US-10-378-393-11 Sequence 11, Appli
15	629	98.0	197	5	US-10-804-762-32 Sequence 32, Appli
16	629	98.0	197	5	US-10-804-763-51 Sequence 51, Appli
17	602	93.8	235	5	US-10-804-763-27 Sequence 27, Appli
18	599	93.3	198	5	US-10-804-762-5 Sequence 5, Appli
19	599	93.3	198	5	US-10-804-763-5 Sequence 5, Appli
20	547	85.2	235	5	US-10-804-762-25 Sequence 25, Appli
21	547	85.2	235	5	US-10-804-763-25 Sequence 25, Appli
22	536	83.5	102	3	US-09-891-119A-13 Sequence 13, Appli
23	366.5	57.1	239	5	US-10-804-762-21 Sequence 21, Appli
24	366.5	57.1	239	5	US-10-804-763-21 Sequence 21, Appli
25	362	56.4	236	5	US-10-804-762-19 Sequence 19, Appli
26	362	56.4	236	5	US-10-804-763-19 Sequence 19, Appli
27	347.5	54.1	242	5	US-10-804-762-17 Sequence 17, Appli

28	347.5	54.1	242	5	US-10-804-763-17	Sequence 17, Appli
29	340	53.0	237	5	US-10-804-762-15	Sequence 15, Appli
30	340	53.0	237	5	US-10-804-763-15	Sequence 15, Appli
31	279.5	43.5	235	5	US-10-804-762-23	Sequence 23, Appli
32	279.5	43.5	235	5	US-10-804-762-23	Sequence 23, Appli
33	248	38.6	236	5	US-10-804-762-13	Sequence 13, Appli
34	248	38.6	236	5	US-10-804-763-13	Sequence 13, Appli
35	239	37.2	310	5	US-10-804-762-7	Sequence 7, Appli
36	239	37.2	310	5	US-10-804-763-7	Sequence 7, Appli
37	238	37.1	247	5	US-10-804-762-11	Sequence 11, Appli
38	238	37.1	247	5	US-10-804-763-11	Sequence 11, Appli
39	238	37.1	247	5	US-10-804-763-50	Sequence 50, Appli
40	238	37.1	207	5	US-10-804-762-9	Sequence 9, Appli
41	232	36.1	207	5	US-10-804-763-9	Sequence 9, Appli
42	232	36.1	207	5	US-10-804-763-9	Sequence 9, Appli
43	229	35.7	310	5	US-10-804-762-29	Sequence 29, Appli
44	229	35.7	310	5	US-10-804-763-29	Sequence 29, Appli
45	139	21.7	444	2	US-08-812-393A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-10-804-762-3  
Sequence 3, Application US/10804762  
Publication No. US20050042217A1  
GENERAL INFORMATION:  
APPLICANT: Qi, Yan  
APPLICANT: Zhang, Xianghua  
APPLICANT: Konigsberg, Paula  
TITLE OF INVENTION: Specific Inhibition of Allorejection  
FILE REFERENCE: A-72186/TAL/DCF (471702-00005)  
CURRENT APPLICATION NUMBER: US/10/804,762  
CURRENT FILING DATE: 2004-03-19  
PRIOR APPLICATION NUMBER: US 60/456,378  
PRIOR FILING DATE: 2003-03-19  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-804-762-3

Query Match 99.2%; Score 637; DB 5; Length 198;  
Best Local Similarity 100.0%; Pred. No. 3e-60;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNLGETVELKCOVLISNPTSGCSWLFOPRGAASPTFLLYLSQNKPKAA 61  
DB 22 SQFRVSPIDRTWNLGETVELKCOVLISNPTSGCSWLFOPRGAASPTFLLYLSQNKPKAA 81

QY 62 EGLDTQRRSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFLPAKPTTTP 121  
DB 82 EGLDTQRRSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFLPAKPTTTP 141

RESULT 2  
US-10-804-763-3  
Sequence 3, Application US/10804763  
Publication No. US20050118676A1  
GENERAL INFORMATION:  
APPLICANT: Qi, Yan  
APPLICANT: Zhang, Xianghua  
APPLICANT: Konigsberg, Paula  
TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity  
FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)  
CURRENT APPLICATION NUMBER: US/10/804,763  
CURRENT FILING DATE: 2004-03-19  
PRIOR APPLICATION NUMBER: US 60/456,378  
PRIOR FILING DATE: 2003-03-19  
NUMBER OF SEQ ID NOS: 51

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-804-763-3
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Query Match          99.2%; Score 637; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
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DB      22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81

QY      62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 121
          |||||||
DB      82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 141
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## RESULT 3

US-10-378-393-20

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; Sequence 20, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-378-393-20
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Query Match          99.2%; Score 637; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
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DB      22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81

QY      62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 121
          |||||||
DB      82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 141
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## RESULT 4

US-10-378-393-3

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; Sequence 3, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
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; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-378-393-3
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Query Match          99.2%; Score 637; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
          |||||||
DB      22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81

QY      62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 121
          |||||||
DB      82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 141
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## RESULT 5

US-10-378-393-13

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; Sequence 13, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-378-393-13
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```
Query Match          99.2%; Score 637; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
          |||||||
DB      22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81

QY      62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 121
          |||||||
DB      82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPLPAKPTTTP 141
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## RESULT 6

US-10-099-007A-6

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; Sequence 6, Application US/10099007A
; Publication No. US20030017150A1
; GENERAL INFORMATION:
; APPLICANT: Theodore Torphy
; TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULMONARY DISEASE-RELATED IMMUNOGLOBULIN
; TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0286
; CURRENT APPLICATION NUMBER: US/10/099,007A
; CURRENT FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 17
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SOFTWARE: PatentIn Ver 2.0  
; SEQ ID NO 6  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-099-007A-6

Query Match 99.2%; Score 637; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3.6e-60;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 61  
|||||  
DB 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 7  
US-10-207-655-174

; Sequence 174, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 174  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-174

Query Match 99.2%; Score 637; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3.6e-60;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 61  
|||||  
DB 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 8  
US-10-723-860-1244

; Sequence 1244, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natabha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1244  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-723-860-1244

Query Match 99.2%; Score 637; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3.6e-60;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 61  
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DB 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 9  
US-10-804-762-1

; Sequence 1, Application US/10804762  
; Publication No. US20050042217A1  
; GENERAL INFORMATION:  
; APPLICANT: Qi, Yan  
; APPLICANT: Zhang, Xianghua  
; APPLICANT: Konigsberg, Paula  
; TITLE OF INVENTION: Specific Inhibition of Allorejection  
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)  
; CURRENT APPLICATION NUMBER: US/10/804,762  
; PRIOR FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: US 60/456,378  
; PRIOR FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-804-762-1

Query Match 99.2%; Score 637; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3.6e-60;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLISQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 10  
US-10-804-762-27

; Sequence 27, Application US/10804762  
; Publication No. US20050042217A1  
; GENERAL INFORMATION:  
; APPLICANT: Qi, Yan  
; APPLICANT: Zhang, Xianghua  
; APPLICANT: Konigsberg, Paula  
; TITLE OF INVENTION: Specific Inhibition of Allorejection  
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)  
; CURRENT APPLICATION NUMBER: US/10/804,762  
; PRIOR FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: US 60/456,378  
; PRIOR FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-804-762-27

Query Match 99.2%; Score 637; DB 5; Length 235;





US-10-378-393-11

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Query Match          99.2%; Score 637; DB 4; Length 791;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 SQFRVSPLDRTWNLGETVBLKQCVLLSNPTSGCSWLFQPRGAAASPFLLYLSQNKPKAA 61  
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Db 22 SQFRVSPLDRTWNLGETVBLKQCVLLSNPTSGCSWLFQPRGAAASPFLLYLSQNKPKAA 81

QY	62	EGLDQRFSGKRLGDTFVLTLSDFRRENEGIFYFCSALNSIMYFSHFVFPVFLPAKPTTTP	121
Db	82	EGLDQRFSGKRLGDTFVLTLSDFRRENEGIFYFCSALNSIMYFSHFVFPVFLPAKPTTTP	141

## RESULT 15

US-10-804-762-32

Sequence 32, Application US/10804762

Publication No. US20050042217A1

GENERAL INFORMATION:

APPLICANT: Q1, Yan

APPLICANT: Zhang, Xianghua

APPLICANT: Konigsberg, Paula  
TITLE OF INVENTION: Snoodies

;; ILLS OF INVENTION: specific inhibition of Allorejection  
: FT.B REFERENCE: A-72196/TAI/DCE (421703-00005)

CURRENT APPLICATION NUMBER: IIS/10/904 253

CURRENT FILING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: IIS 60/

PRIOR FILING DATE: 2003-03-19

NUMBER OF SEQ ID NOS: 32

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; SOFTWARE: PatentIn version 3.2.2

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SEQ ID NO 32

LENGTH: 197

TYPE: PRT

**ORGANISM:** *Homo sapiens*

US-10-804-762-32

Query Match	98.0%	Score 629;	DB 5;	Length 197;
Best Local Similarity	99.2%;	Pred. No. 2.1e-59;		
Matches 119;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKQCQVLNSNPTSGCSWL EQPRGAASPTFLLYLSQNKPKAA 61  
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Db 22 SQFRVSPLDRTWNLGWTVELKQCQVLNSNPTSGCSWL EQPRGAASPTFLLYLSQNKPKAA 81

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Db	82	EGLD	Q	R	F	S	G	K	R	L	G	D	T	P	V	L	T	S	D	F	R	R	E	N	E	G	Y	F	C	S	A	L	S	N	S	I	M	F	S	H	F	V	P	V	F	L	P	A	K	T	T	T	P		141			

Search completed: April 5, 2006, 15:55:07  
Job time : 44 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:52:51 ; Search time 19 Seconds  
(without alignments)  
526.514 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642  
Sequence: 1 MSQFRVSPIDRTWNLGETVE.....IMYFSHFVPVFLPAKPTTTP 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	637	99.2	235	1 US-07-940-605A-12	Sequence 12, Appl
2	637	99.2	235	1 US-08-690-096-12	Sequence 12, Appl
3	637	99.2	376	2 US-08-751-512-8	Sequence 8, Appl
4	603	93.9	114	1 US-08-372-952-1	Sequence 1, Appl
5	603	93.9	114	2 US-08-875-309-1	Sequence 1, Appl
6	603	93.9	114	4 PCT-US96-00310-1	Sequence 1, Appl
7	603	93.9	114	1 US-08-403-853-12	Sequence 12, Appl
8	536	83.5	102	2 US-08-466-368-8	Sequence 8, Appl
9	536	83.5	102	2 US-08-470-998-5	Sequence 5, Appl
10	536	83.5	102	2 US-08-328-500-13	Sequence 13, Appl
11	239	37.2	249	1 US-07-940-605A-10	Sequence 10, Appl
12	239	37.2	249	1 US-08-690-096-10	Sequence 10, Appl
13	228	35.5	280	1 US-08-403-853-10	Sequence 10, Appl
14	227.5	35.4	269	2 US-09-531-056A-14	Sequence 14, Appl
15	227.5	35.4	328	2 US-09-531-056A-13	Sequence 13, Appl
16	227.5	35.4	331	2 US-09-531-056A-12	Sequence 12, Appl
17	135.5	21.1	124	2 US-08-751-359-14	Sequence 14, Appl
18	135.5	21.1	124	2 US-08-907-146-14	Sequence 14, Appl
19	127.5	19.9	105	2 US-10-083-424-32	Sequence 32, Appl
20	122	19.0	108	2 US-10-083-424-30	Sequence 30, Appl
21	120.5	18.8	126	2 US-08-751-359-12	Sequence 12, Appl
22	120.5	18.8	126	2 US-08-907-146-12	Sequence 12, Appl
23	119.5	18.6	235	2 US-09-049-672A-10	Sequence 10, Appl
24	118.5	18.5	108	2 US-09-914-695-34	Sequence 34, Appl
25	117.5	18.3	229	2 US-08-751-359-22	Sequence 22, Appl
26	117.5	18.3	229	2 US-08-907-146-22	Sequence 22, Appl
27	115.5	18.0	104	2 US-10-083-424-40	Sequence 40, Appl

28	113	17.6	104	2 US-10-083-424-28	Sequence 28, Appl
29	113	17.6	112	2 US-10-330-613A-2	Sequence 2, Appl
30	111.5	17.4	108	2 US-10-092-246-19	Sequence 19, Appl
31	111.5	17.4	108	2 US-10-096-246A-19	Sequence 19, Appl
32	111.5	17.4	111	1 US-08-665-202-36	Sequence 36, Appl
33	111.5	17.4	111	2 US-09-315-574-36	Sequence 36, Appl
34	111.5	17.4	113	2 US-09-232-290-20	Sequence 20, Appl
35	111.5	17.4	258	1 US-08-665-202-5	Sequence 5, Appl
36	111.5	17.4	258	2 US-09-315-574-5	Sequence 5, Appl
37	111.5	17.4	262	2 US-09-069-821-4	Sequence 4, Appl
38	111.5	17.4	262	2 US-09-956-086-4	Sequence 4, Appl
39	111.5	17.4	262	2 US-09-956-087-4	Sequence 4, Appl
40	111.5	17.4	282	2 US-09-420-592A-7	Sequence 7, Appl
41	111.5	17.4	282	2 US-09-985-442-7	Sequence 7, Appl
42	111.5	17.4	282	2 US-09-983-580-7	Sequence 7, Appl
43	111	17.3	130	2 US-09-339-596A-28	Sequence 28, Appl
44	110.5	17.2	106	2 US-09-240-274-47	Sequence 47, Appl
45	110.5	17.2	106	2 US-09-848-798-47	Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-07-940-605A-12  
Sequence 12, Application US/07940605A  
Patent No. 5540926  
GENERAL INFORMATION:  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: HOLLENBAUGH, DIANE  
APPLICANT: LEDBETTER, JEFFREY A.  
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/940,605A  
FILING DATE: 04-SEP-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIB  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-940-605A-12

Query Match 99.2%; Score 637; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.8e-64;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 61  
DB 22 SQFRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 81

Qy      62 EGLDQRFSGKRLGDTFVLTLSDFRRNEGYFFCSALNSIMYFSHFVPVFLPAKPPTTP    121

Db      82 EGLDQRFSGKRLGDTFVLTLSDFRRNEGYFFCSALNSIMYFSHFVPVFLPAKPPTTP    141

## RESULT 2

```

US-08-690-096-12
; Sequence 12, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-690-096-12

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Query Match	99.2%	Score 637;	DB 1;	Length 235;
Best Local Similarity	100.0%	Pred. No. 4.8e-64;		
Matches 120; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2	SQFRVSP	LDRTWNLGETVELK	CQVL	SNPTSGC	SWLFQ	PRGAAS	PTFLYL	SNKPKAA	61
Db	22	SQFRVSP	LDRTWNLGETVELK	CQVL	SNPTSGC	SWLFQ	PRGAAS	PTFLYL	SNKPKAA	81
QY	62	EGLDTOR	FSGKRLGDTFVL	TLSD	FRRENGYY	FCSAL	SNSIMY	FSHFV	PVFLPAKPTTP	121
Db	82	EGLDTOR	FSGKRLGDTFVL	TLSD	FRRENGYY	FCSAL	SNSIMY	FSHFV	PVFLPAKPTTP	141

### RESULT 3

US-08-751-512-8  
; Sequence 8, Application US/08751512  
; Patent No. 6001962  
; GENERAL INFORMATION:  
; APPLICANT: Ramer, J. Kevin  
; APPLICANT: Williams, Lewis T.  
; TITLE OF INVENTION: Modified FAS Ligands  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
;

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111

**COMPUTER READABLE FORM:**

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,512
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 02307K-07100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
US-08-751-512-8

```

Query Match	99.2%	Score 637;	DB 2;	Length 376;
Best Local Similarity	100.0%	Pred. No. 8.8e-64;		
Matches 120; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	2	SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFPQPRGAASPFTLLYLSONKPKAA	61
Db	22	SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFPQPRGAASPFTLLYLSONKPKAA	81
QY	62	EGLDQRFSGKRLGDTFVLLTSLDSFRRENEGYFFCSALSNLSIMYFSHFVVPFLPAKPTTP	121
Db	82	EGLDQRFSGKRLGDTFVLLTSLDSFRRENEGYFFCSALSNLSIMYFSHFVVPFLPAKPTTP	141

## RESULT 4

```

US-08-372-952-1
; Sequence 1, Application US/08372952
; Patent No. 5645837
;
; GENERAL INFORMATION:
;
; APPLICANT: Jameson, Bradford A.
;
; APPLICANT: Choksi, Swati
;
; APPLICANT: Korngold, Robert
;
; TITLE OF INVENTION: CD8 Antagonists
;
; NUMBER OF SEQUENCES: 8
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;
; ADDRESSEE: No. 5645837r18
;
; STREET: One Liberty Place, 46th Floor
;
; CITY: Philadelphia
;
; STATE: PA
;
; COUNTRY: USA
;
; ZIP: 19103
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Wordperfect
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/372,952
;
; FILING DATE:
;
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER:
;
; FILING DATE:
;

```



```
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-372-952-1

Query Match          93.9%; Score 603; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGETVELKCVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
Db 1 SQFRVSPDLRTWNLGETVELKCVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 60

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIMYFSHFVPVFLPA 115
Db 61 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIMYFSHFVPVFLPA 114
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## RESULT 5

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US-08-875-309-1
; Sequence 1, Application US/08875309
; Patent No. 6180600
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksi, Swati
; APPLICANT: Korngold, Robert
; APPLICANT: Huang, Ziwei
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,309
; FILING DATE: 26-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00310
; FILING DATE: 17-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,952
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-309-1
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```
Query Match          93.9%; Score 603; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2 SQFRVSPDLRTWNLGETVELKCVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
Db 1 SQFRVSPDLRTWNLGETVELKCVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 60

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIMYFSHFVPVFLPA 115
Db 61 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIMYFSHFVPVFLPA 114
```

## RESULT 6

```
PCT-US96-00310-1
; Sequence 1, Application PC/TUS9600310
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksi, Swati
; APPLICANT: Korngold, Robert
; APPLICANT: Huang, Ziwei
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00310
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,952
; FILING DATE: 17-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-00310-1
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Query Match          93.9%; Score 603; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2 SQFRVSPDLRTWNLGETVELKCVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
Db 1 SQFRVSPDLRTWNLGETVELKCVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 60

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIMYFSHFVPVFLPA 115
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Db 61 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFLPA 114

RESULT 7  
US-08-403-853-12

; Sequence 12, Application US/08403853  
; Patent No. 5844094  
; GENERAL INFORMATION:  
; APPLICANT: HUDSON, Peter J.  
; APPLICANT: LAH, Maria  
; APPLICANT: KORRT, Alex A.  
; APPLICANT: IRVING, Robert A.  
; APPLICANT: ATWELL, John L.  
; APPLICANT: MALBY, Robyn L.  
; APPLICANT: POWER, Barbara E.  
; APPLICANT: COLMAN, Peter M.  
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,853  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/AU93/00491  
; FILING DATE: 24-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PL 4973  
; FILING DATE: 25-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 273 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-403-853-12

Query Match 93.9%; Score 603; DB 1; Length 273;  
Best Local Similarity 100.0%; Pred. No. 4.1e-60;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 61  
Db 23 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 82  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFLPA 115  
Db 83 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFLPA 136

RESULT 8  
US-08-466-368-8  
; Sequence 8, Application US/08466368

; Patent No. 6093539  
; GENERAL INFORMATION:  
; APPLICANT: Maddon, Paul J.  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Chess, Leonard  
; APPLICANT: Axel, Richard  
; APPLICANT: Weiss, Robin  
; APPLICANT: McDougal, J. S.  
; TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN  
; TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,368  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 24577-E1-B/JPW/AKC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
; FEATURE:  
; NAME/KEY: Active-site  
; LOCATION: 1..102  
US-08-466-368-8

Query Match 83.5%; Score 536; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 61  
Db 1 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 60  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIM 103  
Db 61 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIM 102

RESULT 9  
US-08-470-998-5  
; Sequence 5, Application US/08470998  
; Patent No. 6570000  
; GENERAL INFORMATION:  
; APPLICANT: Maddon, Paul J.  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Chess, Leonard  
; APPLICANT: Axel, Richard  
; APPLICANT: Weiss, Robin  
; APPLICANT: McDougal, J. S.  
; TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN

1 TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS  
2 NUMBER OF SEQUENCES: 14  
3 CORRESPONDENCE ADDRESS:  
4 ADDRESSEE: Cooper & Dunham LLP  
5 STREET: 1185 Avenue of Americas  
6 CITY: New York  
7 STATE: New York  
8 COUNTRY: USA  
9 ZIP: 10036  
10 COMPUTER READABLE FORM:  
11 MEDIUM TYPE: floppy disk  
12 COMPUTER: IBM PC compatible  
13 OPERATING SYSTEM: PC-DOS/MS-DOS  
14 SOFTWARE: PatentIn Release #1.0, Version #1.30  
15 CURRENT APPLICATION DATA:  
16 APPLICATION NUMBER: US/08/470,998  
17 FILING DATE: 06-JUN-1995  
18 CLASSIFICATION: 435  
19 ATTORNEY/AGENT INFORMATION:  
20 NAME: White, John P.  
21 REGISTRATION NUMBER: 28,678  
22 REFERENCE/DOCKET NUMBER: 24577-F1-B/JPW/AKC  
23 TELECOMMUNICATION INFORMATION:  
24 TELEPHONE: 212-278-0400  
25 TELEFAX: 212-391-0525  
26 INFORMATION FOR SEQ ID NO: 5:  
27 SEQUENCE CHARACTERISTICS:  
28 LENGTH: 102 amino acids  
29 TYPE: amino acid  
30 STRANDEDNESS: single  
31 TOPOLOGY: linear  
32 MOLECULE TYPE: protein  
33 HYPOTHETICAL: YES  
34 ANTI-SENSE: YES  
35 FEATURE:  
36 NAME/KEY: Active-site  
37 LOCATION: 1..102  
38 US-08-470-998-5  
39  
40 Query Match 83.5%; Score 536; DB 2; Length 102;  
41 Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
42 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
43  
44 QY 2 SQFRVSPIDRTWNLGETVELKCCQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61  
45 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
46 Db 1 SQFRVSPIDRTWNLGETVELKCCQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 60  
47  
48 QY 62 EGLDTQRRSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIM 103  
49 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
50 Db 61 EGLDTQRRSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIM 102  
51  
52 RESULT 10  
53 US-08-328-500-13  
54 Sequence 13, Application US/08328500  
55 Patent No. 6673896  
56 GENERAL INFORMATION:  
57 APPLICANT: Maddon, Paul J.  
58 APPLICANT: Axel, Richard  
59 APPLICANT: Sweet, Richard W.  
60 APPLICANT: Arthos, James  
61 TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4  
62 NUMBER OF SEQUENCES: 22  
63 CORRESPONDENCE ADDRESS:  
64 ADDRESSEE: Cooper & Dunham  
65 STREET: 1185 Avenue of the Americas  
66 CITY: New York  
67 STATE: New York  
68 COUNTRY: U.S.A.  
69 ZIP: 10036  
70 COMPUTER READABLE FORM:  
71 MEDIUM TYPE: floppy disk  
72 COMPUTER: IBM PC compatible

1 OPERATING SYSTEM: PC-DOS/MS-DOS  
2 SOFTWARE: PatentIn Release #1.0, Version #1.30  
3 CURRENT APPLICATION DATA:  
4 APPLICATION NUMBER: US/08/328,500  
5 FILING DATE:  
6 CLASSIFICATION: 435  
7 ATTORNEY/AGENT INFORMATION:  
8 NAME: White, John P.  
9 REGISTRATION NUMBER: 28,678  
10 REFERENCE/DOCKET NUMBER: 0575/24577-CY  
11 TELECOMMUNICATION INFORMATION:  
12 TELEPHONE: (212) 278-0400  
13 TELEFAX: (212) 391-0525  
14 INFORMATION FOR SEQ ID NO: 13:  
15 SEQUENCE CHARACTERISTICS:  
16 LENGTH: 102 amino acids  
17 TYPE: amino acid  
18 STRANDEDNESS: not relevant  
19 TOPOLOGY: not relevant  
20 MOLECULE TYPE: protein  
21 US-08-328-500-13  
22  
23 Query Match 83.5%; Score 536; DB 2; Length 102;  
24 Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
25 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
26  
27 QY 2 SQFRVSPIDRTWNLGETVELKCCQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61  
28 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
29 Db 1 SQFRVSPIDRTWNLGETVELKCCQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 60  
30  
31 QY 62 EGLDTQRRSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIM 103  
32 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
33 Db 61 EGLDTQRRSGKRLGDTFVLTLSDFRRENEGYFCSALSNSIM 102  
34  
35 RESULT 11  
36 US-07-940-605A-10  
37 Sequence 10, Application US/07940605A  
38 Patent No. 5540926  
39 GENERAL INFORMATION:  
40 APPLICANT: ARUFFO, ALEJANDRO  
41 APPLICANT: HOLLENBAUGH, DIANE  
42 APPLICANT: LEDBETTER, JEFFREY A.  
43 TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
44 NUMBER OF SEQUENCES: 15  
45 CORRESPONDENCE ADDRESS:  
46 ADDRESSEE: Pennie & Edmonds  
47 STREET: 1155 Avenue of the Americas  
48 CITY: New York  
49 STATE: New York  
50 COUNTRY: U.S.A.  
51 ZIP: 10036-2711  
52 COMPUTER READABLE FORM:  
53 MEDIUM TYPE: floppy disk  
54 COMPUTER: IBM PC compatible  
55 OPERATING SYSTEM: PC-DOS/MS-DOS  
56 SOFTWARE: PatentIn Release #1.0, Version #1.25  
57 CURRENT APPLICATION DATA:  
58 APPLICATION NUMBER: US/07/940,605A  
59 FILING DATE: 04-SEP-1992  
60 CLASSIFICATION: 530  
61 ATTORNEY/AGENT INFORMATION:  
62 NAME: Mastrock, S. Leslie  
63 REGISTRATION NUMBER: 18,872  
64 REFERENCE/DOCKET NUMBER: 5624-184  
65 TELECOMMUNICATION INFORMATION:  
66 TELEPHONE: 212 790-9090  
67 TELEFAX: 212 869-8864/9741  
68 TELELEX: 66141 PENNIE  
69 INFORMATION FOR SEQ ID NO: 10:  
70 SEQUENCE CHARACTERISTICS:  
71 LENGTH: 249 amino acids  
72 TYPE: amino acid

```

;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
US-07-940-605A-10

```

Query Match	37.2%;	Score 239;	DB 1;	Length 249;
Best Local Similarity	44.7%;	Pred. No. 5.5e-19;		
Matches 55; Conservative	20;	Mismatches 42;	Indels 6;	Gaps 5;

```

QY      3 QFRVSPDLRTMNLGETVEELKCOVLLSNPTSGCSWLFPQPGA--AASPTFLLYL--SQKKPK 59
      : : : : : : : : : : : : : : : : : :
DB     33 ELRIFFPKMDAELGQKVDLVCEV--LGSVSGGCSWLFPQNSSSKLPQTFVVMYMASSHNKIT 91

```

```

QY      60 AAEGIDTOR-FSGKR-LGDTFVLTLSDFRRENEGYYFCASALNSIMYFSHFVPVFLPAKP 117
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      92 WDEKLNSSKLFSAARDTNKKVYLTLNKFSKENEGYYFCSVISNSVMYFSSVVPVLQKYN 151

```

Qy	118	TTT	120
Db	152	TTT	154

RESULT 12  
US-08-690-096-10  
; Sequence 10, Application US/086900096

```

: GENERAL INFORMATION:
: APPLICANT: ARUFFO, ALEJANDRO
: APPLICANT: HOLLENBAUGH, DIANE
: APPLICANT: LEDBETTER, JEFFREY A.
: TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
:

```

```

; ADDRESSSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

!! APPLICATION NUMBER: US/08/690,096  
!! FILING DATE: 31-JUL-1996  
!! CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/940,605  
;; FILING DATE: 04-SEP-1992  
;; ATTORNEY/AGENT INFORMATION:  
;

;  
; NAME: Mastrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

MOLECULE TYPE: peptide  
; US-08-690-096-10

Query Match	37.2%;	Score 239;	DB 1;	Length 249;
Best Local Similarity	44.7%;	Pred. No. 5.5e-19;		
Matches 55;	Conservative 20;	Mismatches 42;	Indels 6;	Gaps 5;

```
QY      3 QFRVSPDLRTWNLGETVELKCOVLISNPFTSGCSWLFPQRGA--AASPTFLLYL--SQNKPK 55
          :|::||::||::||::||::||::||::||::||::||::||:
DB     33 ELRIFFPKMDALGQKVLDVCEV-LGSVSQGCSWLFPQNSSSKLPQTFFVVYMASHNKIT 91
```

```
QY      60 AAEGLDTQR-FSGKR-LGDFEVLTLSDFRRENEGYYFCSALSNISIMYFSHFVEVLELPAPK 117
        |::|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     92 WDEKLNSSKLFPSAMRDITNNKYLTLNKFSKENEGGYFCSVISNVMYSSIVPVLOKVNS 151
```

QY	118	TTT	120
Db	152	TTT	154

RESULT 13  
US-08-403-853-10

; Sequence 10, Application US/08403853

; Patent No. 5844094  
; GENERAL INFORMATION:  
; ADDRESS: YIMCOV Potosi T

APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KOBRT, Alex A.

APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.

APPLICANT: MALBY, Robyn L.  
APPLICANT: POWER, Barbara E.

APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDES

```
; NUMBER OF SEQUENCES:   25  
; CORRESPONDENCE ADDRESS:  
;      00070809T    F-16A C IAWD
```

ADDRESS: Foley & Larnier  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington

CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA

ZIP: 20007-5109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

```
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; PATENT INFORMATION FILE:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995

```

FILED DATE: 30-MAR-1988  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993

;; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PL 4973

FILED DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16706/109/CHAC

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399  
TELEX: 904136

```

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

```

```

;
; LENGTH: 280 amino acids
; TYPE: amino acid
;

```

```

;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
mc 08 403 853 10

```

05-08-403-033-10

Query Match	35.5%;	Score 228;	DB 1;	Length 280;
Best Local Similarity	45.6%;	Pred. No. 1.1e-17;		
Matches 52;	Conservative 20;	Mismatches 36;	Indels 6;	Gaps 5;

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QY      3 QFRVSPDLRTWNLGETVEELKCQVLLSNPTSGCSWLFQPRGA--AASPTFLLYL--SQNPK 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     28 ELRIFPKMDAELGQKYDVLCEV-LGSVSGGCSNLFQNSSKLPQPTFVVVYMAASHNKIT 86

```

```

60 AAEGLDTOR-FSGKR-LGDTFVLTISDFRENEGYYFCSALNSIMYFSHFVPV 111
|:::| | :|::| | :|::|::| | :|::|::| |
QY

```





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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:51:00 ; Search time 51 Seconds  
(without alignments)  
1673.900 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642

Sequence: 1 MSQFRVSPLDRTWNLGETVE.....IMFHFVPEVFLPAKPTTTP 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt\_05.80: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	637	99.2	235	1 CD8A_HUMAN	P01732 homo sapien
2	637	99.2	235	2 Q4ZG17_HUMAN	Q4ZG17 homo sapien
3	631	98.3	235	2 Q96QR6_HUMAN	Q96QR6 homo sapien
4	628	97.8	235	2 Q8TAW8_HUMAN	Q8TAW8 homo sapien
5	599	93.3	198	1 CD8A_PONPY	P30433 pongo pygma
6	547	85.2	235	2 Q9XSM6_SAIISC	Q9XSM6 salmistr sci
7	472	73.5	152	2 Q6ZVS2_HUMAN	Q6ZVS2 homo sapien
8	369.5	57.6	239	1 CD8A_CANPA	P33706 canis famil
9	366.5	57.1	239	1 CD8A_FELCA	P41688 felis silve
10	362	56.4	236	2 Q6GYR4_PIG	Q6GYR4 sus scrofa
11	347.5	54.1	242	1 CD8A_BOVIN	P31783 bos taurus
12	340	53.0	237	2 Q6W8W8_CAVPO	Q6W8W8 cavia porce
13	330	51.4	178	2 Q6R4N4_PIG	Q6R4N4 sus scrofa
14	330	51.4	195	2 Q6R2U9_PIG	Q6R2U9 sus scrofa
15	279.5	43.5	235	2 Q8VH42_SIGHI	Q8VH42 sigmodon hi
16	248	38.6	236	1 CD8A_RAT	P07725 rattus norv
17	239	37.2	222	2 Q8CAX3_MOUSE	Q8CAX3 mus musculu
18	239	37.2	247	1 CD8A_MOUSE	P01731 mus musculu
19	238	37.1	220	2 Q61816_MOUSE	Q61816 mus musculu
20	238	37.1	222	2 Q8C2L1_MOUSE	Q8C2L1 mus musculu
21	238	37.1	247	2 Q60965_MOUSE	Q60965 mus musculu
22	238	37.1	247	2 Q542K6_MOUSE	Q542K6 mus musculu
23	232	36.1	207	2 Q8K2M2_MOUSE	Q8K2M2 mus musculu
24	231	36.0	247	2 Q8C2Q0_MOUSE	Q8C2Q0 mus musculu
25	163.5	25.5	237	2 Q50EU4_CAIMO	Q50EU4 cairina mos
26	155	24.1	235	2 Q90770_CHICK	Q90770 gallus gall
27	154	24.0	235	2 Q6QR62_CHICK	Q6QR62 gallus gall
28	153	23.8	167	2 P79985_CHICK	P79985 gallus gall
29	153	23.8	235	2 Q6QR65_CHICK	Q6QR65 gallus gall
30	152.5	23.8	237	2 Q50EU6_ANAPL	Q50EU6 anas platyr
31	151.5	23.6	237	2 Q90W11_ANAPL	Q90W11 anas platyr

32	151	23.5	167	2 P79986_CHICK	P79986 gallus gall
33	151	23.5	235	2 Q6QR63_CHICK	Q6QR63 gallus gall
34	151	23.5	235	2 Q6QR64_CHICK	Q6QR64 gallus gall
35	147	22.9	235	2 Q6R133_CHICK	Q6R133 gallus gall
36	119.5	18.6	98	2 Q5NV86_HUMAN	Q5NV86 homo sapien
37	119	18.5	99	2 Q5NV65_HUMAN	Q5NV65 homo sapien
38	117.5	18.3	113	1 LV1_CHICK	P04210 gallus gall
39	117.5	18.3	266	2 Q566X2_BRARE	Q566X2 brachydantio
40	116.5	18.1	233	2 Q6GMW4_HUMAN	Q6GMW4 homo sapien
41	113.5	17.7	239	2 Q6P491_HUMAN	Q6P491 homo sapien
42	111.5	17.4	108	1 KV5S_MOUSE	P01652 mus musculu
43	110	17.1	99	2 Q5NV63_HUMAN	Q5NV63 homo sapien
44	110	17.1	236	2 Q6P5S3_HUMAN	Q6P5S3 homo sapien
45	109.5	17.1	113	1 KV2G_MOUSE	P01631 mus musculu

## ALIGNMENTS

RESULT 1	ID	CD8A_HUMAN	STANDARD;	PRT;	235 AA.
AC	P01732	Q13970;			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	13-SEP-2005	(Rel. 48, Last annotation update)			
DE	T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/Leu-2).				
GN	Name=CD8A; Synonyms=MAL;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
OX	[1]				
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).				
RP	MEDLINE=85099337; PubMed=3871356; DOI=10.1016/0092-8674(85)90138-2;				
RX	Littman D.R., Thomas Y., Maddon P.J., Chess L., Axel R.;				
RA	"The isolation and sequence of the gene encoding T8: a molecule defining functional classes of T lymphocytes.";				
RT	Cell 40:237-246(1985).				
RL	[2]				
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).				
RP	MEDLINE=85124610; PubMed=3918796; DOI=10.1016/0092-8674(85)90207-7;				
RX	Sukhatme V.P., Sizer K.C., Vollmer A.C., Hunkapiller T., Parnes J.R.;				
RA	"Structure of Leu-2/T8 as deduced from the sequence of a cDNA clone.";				
RT	Behring Inst. Mitt. 77:48-55(1985).				
RL	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RP	MEDLINE=90035142; PubMed=2509342;				
RX	Nakayama K.-I., Tokito S., Okumura K., Nakauchi H.;				
RA	"Structure and expression of the gene encoding CD8 alpha chain (Leu-2/T8).";				
RT	Immunogenetics 30:393-397(1989).				
RL	[5]				
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2), AND ALTERNATIVE SPLICING.				
RP	MEDLINE=89215302; PubMed=2496167;				
RX	Norment A.M., Lonberg N., Lacy E., Littman D.R.;				
RA	"Alternately spliced mRNA encodes a secreted form of human CD8 alpha. Characterization of the human CD8 alpha gene.";				
RT	J. Immunol. 142:3312-3319(1989).				
RL	[6]				
RP	NUCLEOTIDE SEQUENCE OF 168-235 (ISOFORMS 1 AND 2).				
RP	MEDLINE=89128905; PubMed=2536941;				
RX	Giblin P., Ledbetter J.A., Kavathas P.;				
RA	"A secreted form of the human lymphocyte cell surface molecule CD8				

RT arises from alternative splicing.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:998-1002(1989).  
RN [7]  
RP SUBUNIT.  
RX MEDLINE=84061928; PubMed=6605969;  
RA Snow P.M., Terhorst C.;  
RT "The T8 antigen is a multimeric complex of two distinct subunits on  
human thymocytes but consists of homomultimeric forms on peripheral  
blood T lymphocytes.";  
RL J. Biol. Chem. 258:14675-14681(1983).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 22-135.  
RX MEDLINE=92191292; PubMed=1547508; DOI=10.1016/0092-8674(92)90085-Q;  
RA Leahy D.J., Axel R., Hendrickson W.A.;  
RT "Crystal structure of a soluble form of the human T cell coreceptor  
CD8 at 2.6-A resolution.";  
RL Cell 68:1145-1162(1992).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 22-141 IN COMPLEX WITH  
HLA-A/B2M DIMER.  
RX MEDLINE=97320504; PubMed=9177355; DOI=10.1038/42523;  
RA Gao G.F., Tormo J., Gerth U.C., Weyer J.R., McMichael A.J.,  
RT Stuart D.I., Bell J.I., Jones E.Y., Jakobsen B.K.;  
RT "Crystal structure of the complex between human CD8alpha(alpha) and  
HLA-A2.";  
RL Nature 387:630-634(1997).  
RN [10]  
RP STRUCTURE BY NMR OF 209-227 IN COMPLEX WITH LCK.  
RX MEDLINE=22864827; PubMed=14500983; DOI=10.1126/science.1085643;  
RA Kim P.W., Sun Z.Y., Blacklow S.C., Wagner G., Eck M.J.;  
RT "A zinc clasp structure tethers Lck to T cell coreceptors CD4 and  
CD8.";  
RL Science 301:1725-1728(2003).  
RV [11]  
RP VARIANT CD8 DEFICIENCY SER-111, AND MUTAGENESIS OF GLY-111.  
RX MEDLINE=21329138; PubMed=11435463;  
RA de la Calle-Martin O., Hernandez M., Ordi J., Casamitjana N.,  
RA Arostegui J.I., Caragol I., Ferrando M., Labrador M.,  
RA Rodriguez-Sanchez J.L., Espanol T.;  
RT "Familial CD8 deficiency due to a mutation in the CD8 alpha gene.";  
RL J. Clin. Invest. 108:117-123(2001).  
CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact  
with MHC class I bearing targets. CD8 is thought to play a role in  
the process of T-cell mediated killing. CD8 alpha chains binds to  
class I MHC molecules alpha-3 domains.  
CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain  
linked by two disulfide bonds. Can also form homodimers. Shown to  
be expressed as heterodimer on thymocytes and as homodimer on  
peripheral blood T lymphocytes. Interacts with the MHC class I  
HLA-A/B2M dimer. Interacts with LCK in a zinc-dependent manner.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and  
secreted (isoform 2).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=membrane, mCD8alpha;  
CC IsoId=P01732-1; Sequence=Displayed;  
CC Name=2; Synonyms=secreted, sCD8alpha;  
CC IsoId=P01732-2; Sequence=VSP\_012653;  
CC -1- PTM: All of the five most carboxyl-terminal cysteines form inter-  
chain disulfide bonds in dimers and higher multimers, while the  
four N-terminal cysteines do not (By similarity).  
CC -1- DISEASE: Defects in CD8A are a cause of familial CD8 deficiency  
(CD8 deficiency) [MIM:608957]. Familial CD8 deficiency is a novel  
autosomal recessive immunologic defect characterized by absence of  
CD8+ cells, leading to recurrent bacterial infections.  
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
domain.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.

CC -----  
DR EMBL; M26315; AAA79217.1; -; Genomic DNA.  
DR EMBL; M26313; AAA79217.1; JOINED; Genomic DNA.  
DR EMBL; M26314; AAA79217.1; JOINED; Genomic DNA.  
DR EMBL; M26315; AAA79218.1; -; Genomic DNA.  
DR EMBL; M26313; AAA79218.1; JOINED; Genomic DNA.  
DR EMBL; M26314; AAA79218.1; JOINED; Genomic DNA.  
DR EMBL; M12824; AAA61133.1; -; mRNA.  
DR EMBL; M12828; AAB04637.1; -; mRNA.  
DR EMBL; M27161; AAB59674.1; -; Genomic DNA.  
DR PIR; A30604; RMHUT8.  
DR PDB; 1AKJ; X-ray; D/E=22-141.  
DR PDB; 1CD8; X-ray; @=-.  
DR PDB; 1Q69; NMR; A=209-227.  
DR Ensembl; ENSG00000153563; Homo sapiens.  
DR HGNC; HGNC:1706; CD8A.  
DR MIM; 186910; -.  
DR MIM; 608957; -.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0042101; C:T cell receptor complex; NAS.  
DR GO; GO:0015026; F:coreceptor activity; NAS.  
DR GO; GO:0042288; F:MHC class I protein binding; NAS.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0019882; P:antigen presentation; NAS.  
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.  
DR GO; GO:0042110; P:T cell activation; NAS.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NAS.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW 3D-structure; Alternative splicing; Disease mutation; Immune response;  
KW Immunoglobulin domain; Phosphorylation; Signal; T-cell; Transmembrane.  
FT SIGNAL 1 21  
FT CHAIN 22 235  
FT FT  
FT TOPO\_DOM 22 182  
FT TRANSMEM 183 203  
FT TOPO\_DOM 204 235  
FT DOMAIN 22 135  
FT DISULFID 43 115  
FT VARSPPLIC 172 209  
FT FT  
FT VARIANT 111 111  
FT FT  
FT FT  
FT MUTAGEN 111 111  
FT STRAND 24 27  
FT TURN 35 36  
FT STRAND 39 45  
FT STRAND 54 59  
FT STRAND 68 73  
FT STRAND 79 80  
FT TURN 82 83  
FT TURN 86 88  
FT STRAND 89 94  
FT TURN 95 96  
FT STRAND 97 102  
FT HELIX 107 109  
FT STRAND 111 119  
FT TURN 120 121  
FT STRAND 122 125  
FT STRAND 129 131  
SQ SEQUENCE 235 AA; 25729 MW; FCCA29BAA73726BB CRC64;  
Query Match 99.2%; Score 637; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 9.9e-61;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SQFRVSPLDRTWNLGETVBLKCQVLLSNPTSGCSWLFQPRGAASPFLLYLSQNKPKAA 61  
DB 22 SQFRVSPLDRTWNLGETVBLKCQVLLSNPTSGCSWLFQPRGAASPFLLYLSQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

## RESULT 2

Q4ZG17 HUMAN  
ID Q4ZG17\_HUMAN PRELIMINARY; PRT; 235 AA.  
AC Q4ZG17;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein CD8A.  
GN Name=CD8A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RA Kruchowski S., Haakenson W., Boyer E.;  
RT "The sequence of Homo sapiens BAC clone RP11-81F3."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.H.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Wilson R.K.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC064848; AAX88864.1; -; Genomic\_DNA.  
DR SMR; Q4ZG17; 22-135.  
DR Ensembl; ENSG00000153563; Homo sapiens.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 235 AA; 25729 MW; FCCA298AA73726BB CRC64;

Query Match 99.2%; Score 637; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 9.9e-61;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNIGETVELKCOVLNSPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61  
|||||  
DB 22 SQFRVSPIDRTWNIGETVELKCOVLNSPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 81  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

## RESULT 3

Q96QR6 HUMAN  
ID Q96QR6\_HUMAN PRELIMINARY; PRT; 235 AA.  
AC Q96QR6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mutant CD8 alpha antigen.  
GN Name=CD8A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21329138; PubMed=11435463;  
RA de la Calle-Martin O., Hernandez M., Ordi J., Casamitjana N.,  
RA Arostegui J.I., Caragol I., Ferrando M., Labrador M.,  
RA Rodriguez-Sanchez J.L., Espanol T.;  
RT "Familial CD8 deficiency due to a mutation in the CD8 alpha gene."  
RL J. Clin. Invest. 108:117-123(2001).  
DR EMBL; AY039664; AAK72403.1; -; mRNA.  
DR HSSP; P01732; 1CD8.  
DR SMR; Q96QR6; 22-135.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 235 AA; 25759 MW; FCCA347AAEF732BB CRC64;

Query Match 98.3%; Score 631; DB 2; Length 235;  
Best Local Similarity 99.2%; Pred. No. 4.4e-60;  
Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNIGETVELKCOVLNSPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61  
|||||  
DB 22 SQFRVSPIDRTWNIGETVELKCOVLNSPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 81  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
|||||  
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

## RESULT 4

Q8TAW8 HUMAN  
ID Q8TAW8\_HUMAN PRELIMINARY; PRT; 235 AA.  
AC Q8TAW8;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CD8 antigen alpha polypeptide, isoform 1.  
GN Name=CD8A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]



```
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025715; AAH25715.1; -, mRNA.
DR HSSP; P01732; 1CD8.
DR SMR; Q8TAW8; 22-135.
DR Ensembl; ENSG00000153563; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 235 AA; 25669 MW; FCDFC9B5472D26BB CRC64;

Query Match          97.8%; Score 628; DB 2; Length 235;
Best Local Similarity 99.2%; Pred. No. 9.4e-60;
Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
   |||
Db 22 SQFRVSPLDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81
   |||

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFPVFLPAKPTTP 121
   |||
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFPVFLPAKPTTP 141
   |||

RESULT 5
CD8A_PONPY
ID CD8A_PONPY STANDARD; PRT; 198 AA.
AC P30433;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte
DE differentiation antigen T8/Leu-2).
GN Name=CD8A;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Isolate Jari;
RX MEDLINE=92307742; PubMed=1612644; DOI=10.1007/BF00215289;
RA Lawlor D.A., Parham P.;
RT "Structure of CD8 alpha and beta chains of the orangutan: novel
RT patterns of mRNA splicing encoding hingeless polypeptides.";
RL Immunogenetics 36:121-125(1992).
CC -!- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
CC with MHC class I bearing targets. CD8 is thought to play a role in
CC the process of T-cell mediated killing. CD8 alpha chains binds to
CC class I MHC molecules alpha-3 domains.
CC -!- SUBUNIT: In general heterodimer of an alpha and a beta chain
CC linked by two disulfide bonds. Can also form homodimers.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X60223; CAA42784.1; -, mRNA.
DR PIR; S25656; S25656.
DR HSSP; P01732; 1CD8.
DR SMR; P30433; 22-134.
DR GO; GO:0042101; C:T cell receptor complex; ISS.
DR GO; GO:0015026; F:coreceptor activity; ISS.
```

```
DR GO; GO:0042288; F:MHC class I protein binding; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0042110; P:T cell activation; ISS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immune response; Immunoglobulin domain; Signal; T-cell; Transmembrane.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 198 T-cell surface glycoprotein CD8 alpha
FT chain.
FT TOPO_DOM 22 145 Extracellular (Potential).
FT TRANSMEM 146 166 Potential.
FT TOPO_DOM 167 198 Cytoplasmic (Potential).
FT DOMAIN 22 135 Ig-like V-type.
FT DISULFID 43 115 By similarity.
SQ SEQUENCE 198 AA; 22099 MW; F3EC093EADB05561 CRC64;

Query Match          93.3%; Score 599; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
   |||
Db 22 SQFRVSPLDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81
   |||

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFPVFLP 114
   |||
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVFPVFLP 134
   |||

RESULT 6
Q9XSM6_SAISC
ID Q9XSM6_SAISC PRELIMINARY; PRT; 235 AA.
AC Q9XSM6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD8 alpha chain precursor.
DE Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=92039;
RX MEDLINE=9293362; PubMed=1036934; DOI=10.1007/s002510050672;
RA Ureta-Vidal A., Garcia Z., Lemonnier F.A., Kazanji M.;
RT "Molecular characterization of cDNAs encoding squirrel monkey (Saimiri
RT sciureus) CD8 alpha and beta chains.";
RL Immunogenetics 49:718-721(1999).
DR EMBL; AJ130818; CAB41462.1; -, mRNA.
DR HSSP; P01732; 1CD8.
DR SMR; Q9XSM6; 22-135.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 235 CD8 alpha chain.
SQ SEQUENCE 235 AA; 25728 MW; 055867CD503C268D CRC64;

Query Match          85.2%; Score 547; DB 2; Length 235;
Best Local Similarity 82.5%; Pred. No. 5.9e-51;
Matches 99; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
   |||
Db 22 SQFRVSPLDRTWNIGDKVELKCEVLLSNPSSGCSWLFQPRGAAASPTFLLYISQTKPKYA 81
   |||
```

QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSTMYFSHFVPLPAKPTTP 121  
 Db 82 DGLDAQRFGSGKMGDSFILTLADFRREDQGFYFCSALSNSTMYFSHFVPLPAKPTTP 141

RESULT 7

Q6ZVS2 HUMAN  
 ID Q6ZVS2 HUMAN PRELIMINARY; PRT; 152 AA.  
 AC Q6ZVS2;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Hypothetical protein FLJ42162.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,  
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,  
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,  
 RA Masuho Y., Nagai K., Isogai T.,  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK124156; BAC65789.1; -; mRNA.  
 DR SMR; Q6ZVS2; 63-152.  
 SQ SEQUENCE 152 AA; 16713 MW; 6911F40F86122E02 CRC64;

Query Match 73.5%; Score 472; DB 2; Length 152;  
 Best local similarity 100.0%; Pred. No. 5e-43;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 61  
 Db 63 SQFRVSPDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 122  
 QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENEG 91  
 Db 123 EGLDQRFSGKRLGDTFVLTLSDFRRENEG 152

RESULT 8

CD8A\_CANFA  
 ID CD8A\_CANFA STANDARD; PRT; 239 AA.  
 AC P33706;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE T-cell surface glycoprotein CD8 alpha chain precursor.  
 GN Name=CD8A;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Beagle; TISSUE=Thymus;  
 RA MEDLINE=94378217; PubMed=8091416;  
 RA Gorman S.D., Frewin M.R., Cobbold S.P., Waldmann H.,  
 RT "Isolation and expression of cDNA encoding the canine CD4 and CD8  
 RT alpha antigens."  
 RL Tissue Antigens 43:184-188(1994).  
 CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact  
 CC with MHC class I bearing targets. CD8 is thought to play a role in  
 CC the process of T-cell mediated killing. CD8 alpha chains binds to  
 CC class I MHC molecules alpha-3 domains.

CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain  
 CC linked by two disulfide bonds. Can also form homodimers.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
 CC domain.

CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----  
 CC EMBL; L14287; AAB02294.1; -; mRNA.  
 CC HSSP; P01732; 1CD8.  
 CC DR Ensembl; ENSCAFG0000007464; Canis familiaris.  
 CC DR GO; GO:0042101; C:T cell receptor complex; ISS.  
 CC DR GO; GO:0015026; F:coreceptor activity; ISS.  
 CC DR GO; GO:0042288; F:MHC class I protein binding; ISS.  
 CC DR GO; GO:0005515; F:protein binding; ISS.  
 CC DR GO; GO:0006955; P:immune response; ISS.  
 CC DR GO; GO:0042110; P:T cell activation; ISS.  
 CC DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.  
 CC DR InterPro; IPR007110; Ig-like.  
 CC DR InterPro; IPR003596; Ig\_v.  
 CC DR SMART; SM00406; IGV; 1.  
 CC DR PROSITE; PS50835; IG\_LIKE; 1.  
 CC DR Glycoprotein; Immune\_response; Immunoglobulin domain; Signal; T-cell;  
 CC KW Transmembrane.  
 CC FT SIGNAL 1 21 Potential.  
 CC FT CHAIN 22 239 T-cell surface glycoprotein CD8 alpha  
 CC FT chain.  
 CC FT TOPO\_DOM 22 186 Extracellular (Potential).  
 CC FT TRANSMEM 187 210 Potential.  
 CC FT TOPO\_DOM 211 239 Cytoplasmic (Potential).  
 CC FT DOMAIN 25 139 Ig-like V-type.  
 CC FT CARBOHYD 156 156 N-linked (GlcNAc. .) (Potential).  
 CC FT DISULFID 46 119 By similarity.  
 CC SQ SEQUENCE 239 AA; 26036 MW; 1018579779A5CB7B CRC64;

Query Match 57.6%; Score 369.5; DB 1; Length 239;  
 Best local similarity 60.3%; Pred. No. 1.2e-31;  
 Matches 73; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

QY 2 SQFRVSPDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 61  
 Db 25 SFRMTPEPKVVGQIHAQVELQCQVLLSTAAPGCSWLYGRNEPARPVFLMYISQSRAPKA 84  
 QY 62 EGLDQRFSG-KRLGDTFVLTLSDFRRENEGYYFCSALSNSTMYFSHFVPLPAKPTTP 120  
 Db 85 EGLDQRFSG-KRLGDTFVLTLSDFRRENEGYYFCSALSNSTMYFSHFVPLPAKPTTP 144

QY 121 P 121  
 Db 145 P 145

RESULT 9

CD8A\_FELCA  
 ID CD8A\_FELCA STANDARD; PRT; 239 AA.  
 AC P41688;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE T-cell surface glycoprotein CD8 alpha chain precursor.  
 GN Name=CD8A;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
 OC Felinae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;

```

RX MEDLINE=94178799; PubMed=8132208;
RA Pecoraro M., Kawaguchi Y., Miyazawa T., Norimine J., Maeda K.,
RA Toyosaki T., Tohya Y., Kai C., Mikami T.;
RT "Isolation, sequence and expression of a cDNA encoding the alpha-chain
RT of the feline CD8.";
RL Immunology 81:127-131 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA Miyazawa T.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
CC with MHC class I bearing targets. CD8 is thought to play a role in
CC the process of T-cell mediated killing. CD8 alpha chains binds to
CC class I MHC molecules alpha-3 domains.
CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain
CC linked by two disulfide bonds. Can also form homodimers.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, D16536; BAA03973.1; -; mRNA.
DR EMBL, AB000485; BAA19126.1; -; mRNA.
DR PIR, I46082; I46082.
DR HSSP, P01732; 1CD8.
DR GO, GO:0042101; C:T cell receptor complex; ISS.
DR GO, GO:0015026; F:coreceptor activity; ISS.
DR GO, GO:0042288; F:MHC class I protein binding; ISS.
DR GO, GO:0005515; F:protein binding; ISS.
DR GO, GO:0006955; P:immune response; ISS.
DR GO, GO:0042110; P:T cell activation; ISS.
DR GO, GO:0007169; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro, IPR003599; Ig.
DR InterPro, IPR007110; Ig-like.
DR Pfam, PF00047; Ig; 1.
DR SMART, SMO0409; IG; 1.
DR PROSITE, PS50835; IG LIKE; 1.
FT IMMUNE response; Immunoglobulin domain; Signal; T-cell; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 239 T-cell surface glycoprotein CD8 alpha chain.
FT FT
FT TOPO DOM 22 188 Extracellular (Potential).
FT TRANSMEM 189 210 Potential.
FT TOPO DOM 211 239 Cytoplasmic (Potential).
FT DOMAIN 25 139 Ig-like V-type.
FT DISULFID 46 119 By similarity.
FT SEQUENCE 239 AA; 26120 MW; F9A171820E8FF1BC CRC64;
QY Query Match 57.1%; Score 366.5; DB 1; Length 239;
QY Best Local Similarity 58.7%; Pred. No. 2.5e-31;
QY Matches 71; Conservative 19; Mismatches 30; Indels 1; Gaps 1;
DB 25 SPFRLLSPVRVEGRLLGQRVELQCEVLSSAAGCTWLFOKNEPARPIFLAYLSRSRTKLA 84
QY 62 EGLDQRFSGKRLGDT-FVLTLSDFRRENEGYYFCSALNSNSIMYFSHFVPVFLPAKPTTT 120
DB 85 EELDPKQISGQRIQDTLYSLTLHRRKEEGYYFCSSVNSNVLVPSAFVVPVFLPVKPTTT 144
QY 121 P 121
DB 145 P 145

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ID Q6GYR4_PIG PRELIMINARY; PRT; 236 AA.
AC Q6GYR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD8 antigen alpha protein.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang J., Yang H., Guo X.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY590798; AAT52341.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin domain.
KM SEQUENCE 236 AA; 26329 MW; FFE3887E155EF7EC CRC64;
SQ
Query Match 56.4%; Score 362; DB 2; Length 236;
Best Local Similarity 57.5%; Pred. No. 7.5e-31;
Matches 69; Conservative 19; Mismatches 32; Indels 0; Gaps 0;

QY 2 SQPRVSPLDRTWNIGETVELKQVLSNPTSGCSWLFPQPGAASPTFLYLSONKPKAA 61
| | | | | : | | | | | : | | | | | : | | | | | : | |
| | | | | : | | | | | : | | | | | : | | | | | : | |
25 SLFRTPSPMVOASIGETVELQCELMHSNLTSCSWLYQKPGAASKPIFLMYLSKTRNKTA 84

QY 62 EGLDTRQFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTP 121
| | | | | : | | | | | : | | | | | : | | | | | : | |
| | | | | : | | | | | : | | | | | : | | | | | : | |
85 EGLDTRYISGYKANDNPFYLLHRFREEDQGYFCFSFLNSVLYFSNFMVSFLPAKPTKTP 144

Db
Db 85 EGLDTRYISGYKANDNPFYLLHRFREEDQGYFCFSFLNSVLYFSNFMVSFLPAKPTKTP 144

RESULT 11
CD8A_BOVIN
ID CD8A_BOVIN STANDARD; PRT; 242 AA.
AC P31783;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE T-cell surface glycoprotein CD8 alpha chain precursor.
OS Name=CD8A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Thymus;
RX MEDLINE=92332098; PubMed=1628904;
RA Lalor P., Buccì C., Fornaro M., Rattazzi M.C., Nakauchi H.,
RA Herzenberg L.A., Alberti S.;
RT "Molecular cloning, reconstruction and expression of the gene encoding
RT the alpha-chain of the bovine CD8 -- definition of three peptide
RT regions conserved across species.";
RL Immunology 76:95-102(1992).
CC -!- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
CC with MHC class I bearing targets. CD8 is thought to play a role in
CC the process of T-cell mediated killing. CD8 alpha chains binds to
CC class I MHC molecules alpha-3 domains.
CC -!- SUBUNIT: In general heterodimer of an alpha and a beta chain
CC linked by two disulfide bonds. Can also form homodimers.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC -----  
DR EMBL; X59416; CAA42051.1; -; mRNA.  
DR PIR; S25663; S25663.  
DR HSSP; P01732; 1CD8.

DR GO; GO:0042101; C:T cell receptor complex; ISS.  
DR GO; GO:0015026; F:coreceptor activity; ISS.  
DR GO; GO:0042288; F:MHC class I protein binding; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0006955; P:immune response; ISS.  
DR GO; GO:0042110; P:T cell activation; ISS.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immune response; Immunoglobulin domain; Signal; T-cell; Transmembrane.  
FT SIGNAL 1 25 Potential.  
FT CHAIN 26 242 T-cell surface glycoprotein CD8 alpha chain.  
FT FT TOPO\_DOM 26 189 Extracellular (Potential).  
FT TRANSMEM 190 214 Potential.  
FT TOPO\_DOM 215 242 Cytoplasmic (Potential).  
FT DOMAIN 26 140 Ig-like V-type.  
FT DISULFID 47 120 By similarity.  
SQ SEQUENCE 242 AA; 26417 MW; 91481320EF05195E CRC64;

Query Match 54.1%; Score 347.5; DB 1; Length 242;  
Best Local Similarity 57.1%; Pred. No. 2.9e-29;  
Matches 68; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

Qy 4 FRVSPIDRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAAEG 63  
Db 28 FRMSPTQKETRLGKVELQCELLQSGMATGCSWLRHIPGDDPRPTFLMYLSAQRVKLAEG 87  
Qy 64 LDTQRFSGKRL-GDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 88 LDPRHISGAKVSGTKFQTLTSSFLQEDQGYFCSVSVNSILYFSNFVFPVFLPAKPATTP 146

## RESULT 12

Q6W8W8\_CAVPO  
ID Q6W8W8\_CAVPO PRELIMINARY; PRT; 237 AA.  
AC Q6W8W8;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DB CD8 alpha.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;  
OC Hystriocognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14705990; DOI=10.1111/j.1399-0039.2004.00155.x;  
RA Nagarajan U.M., O'Connell C., Rank R.G.;  
RT "Molecular characterization of guinea - pig (Cavia porcellus) CD8alpha  
RT and CD8beta cDNA."  
RL Tissue Antigens 63:184-189(2004).  
DR EMBL; AY303773; AAQ73501.1; -; mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 237 AA; 25627 MW; 5358FDAD87D6A9B6 CRC64;

Query Match 53.0%; Score 340; DB 2; Length 237;  
Best Local Similarity 53.3%; Pred. No. 1.8e-28;  
Matches 64; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

Qy 2 SQFRVSPIDRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAA 61  
Db 27 SQFRMSPRELVAQVGTKVTLRCVLPVNPAPAGCSWLFQPRHDAKPTFLYHSASGTCLA 86  
Qy 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 87 PGLQKRFSPSKSSNTYTLTVNSFQKRDEGYFCSVSGNMMLYFSPFVPVFLPAPRTTTP 146

## RESULT 13

Q6R4N4\_PIG  
ID Q6R4N4\_PIG PRELIMINARY; PRT; 178 AA.  
AC Q6R4N4;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE CD8 antigen alpha polypeptide (Fragment).  
GN Name=CD8A;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang J., Yang H., Guo X.;  
RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY514489; AAR98817.1; -; mRNA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 178 178  
SQ SEQUENCE 178 AA; 20160 MW; AD373258B32D9BB1 CRC64;

Query Match 51.4%; Score 330; DB 2; Length 178;  
Best Local Similarity 58.3%; Pred. No. 1.6e-27;  
Matches 60; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Qy 19 VELKQVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKAEGLDTRFSGKRLGDTF 78  
Db 1 VELQCELHMSNTLTSCSWLYQKPGAASKPIFLMYLSKTRNKTAEGLDTRYISGYKANDNF 60  
Qy 79 VLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 61 YLTIHRFREDDQGYFCSFLSNVLYFSNFMVSFVFLPAKPTKTP 103

## RESULT 14

Q6R2U9\_PIG  
ID Q6R2U9\_PIG PRELIMINARY; PRT; 195 AA.  
AC Q6R2U9;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE CD8 antigen alpha protein (Fragment).  
GN Name=CD8A;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang J., Yang H., Guo X.;  
RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY517855; AAS01522.1; -; mRNA.  
DR InterPro; IPR007110; Ig-like.







GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:50:39 ; Search time 81 Seconds  
(without alignments)  
656.356 Million cell updates/sec

Title: US-09-560-494E-24  
Perfect score: 642  
Sequence: 1 MSQFRVSPIDRTWNLGETVE.....IMYFSHFVPVFLPAKPTTP 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642	100.0	121	2	AAY21689
2	637	99.2	198	8	ADS92792
3	637	99.2	198	8	ADS19438
4	637	99.2	198	9	ADZ26404
5	637	99.2	235	2	AAR49550
6	637	99.2	235	2	AAY21688
7	637	99.2	235	5	ABP54792
8	637	99.2	235	6	AAO19807
9	637	99.2	235	7	ADD25613
10	637	99.2	235	8	ADP12470
11	637	99.2	235	8	ADQ18425
12	637	99.2	235	8	ADS92816
13	637	99.2	235	8	ADS92790
14	637	99.2	235	8	ADS19436
15	637	99.2	235	9	ADZ26402
16	637	99.2	376	3	AAY52588
17	634	98.8	120	6	AAO19808
18	634	98.8	235	6	AAO19809
19	629	98.0	197	8	ADS92789
20	603	93.9	114	2	AAR98514
21	603	93.9	114	3	AAY43644
22	603	93.9	273	2	AAR52862
23	599	93.3	198	8	ADS92794
24	599	93.3	198	8	ADS19440

25	547	85.2	235	8	ADS92814	AdS92814 Amino aci
26	547	85.2	235	8	ADS19460	AdS19460 Common sq
27	472	73.5	152	8	ADQ66821	AdQ66821 Novel hum
28	366.5	57.1	239	8	ADS92810	AdS92810 Amino aci
29	366.5	57.1	239	8	ADS19456	AdS19456 Cat CD8 a
30	347.5	54.1	242	8	ADS92806	AdS92806 Amino aci
31	347.5	54.1	242	8	ADS19452	AdS19452 Cow CD8 a
32	340	53.0	237	8	ADS92804	AdS92804 Amino aci
33	340	53.0	237	8	ADS19450	AdS19450 Guinea pi
34	330	51.4	195	8	ADS92808	AdS92808 Amino aci
35	330	51.4	195	8	ADS19454	AdS19454 Domestic
36	279.5	43.5	235	8	ADS92812	AdS92812 Hispid co
37	279.5	43.5	235	8	ADS19458	AdS19458 Amino aci
38	248	38.6	236	8	ADS92802	AdS92802 Amino aci
39	248	38.6	236	8	ADS19448	AdS19448 Rat CD8 a
40	239	37.2	130	2	AAY21691	Aay21691 Expressed
41	239	37.2	247	2	AAY21690	Aay21690 Mouse CD8
42	239	37.2	282	2	AAR49549	Aar49549 Sequence
43	239	37.2	310	8	ADS92818	AdS92818 Amino aci
44	239	37.2	310	8	ADS92796	AdS92796 Amino aci
45	239	37.2	310	8	ADS19442	AdS19442 Murine CD

ALIGNMENTS

RESULT 1  
AAY21689  
ID AAY21689 standard; protein; 121 AA.  
XX  
AC AAY21689;  
XX  
DT 18-AUG-1999 (first entry)  
XX  
DE Expressed fragment of human CD8 alpha protein.  
XX  
KW T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;  
KW autoimmune disease; allergy; asthma; viral infection; cytotoxic;  
KW corticosteroid; human; CD8 alpha protein.  
XX  
OS Homo sapiens.  
XX  
PN WO9921576-A1.  
XX  
PD 06-MAY-1999.  
XX  
PF 28-OCT-1998; 98WO-GB003235.  
XX  
PR 28-OCT-1997; 97GB-00022779.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Jakobsen BK, Gao GF, Gerth UC, Sewell AK;  
XX  
DR WPI; 1999-385058/32.  
DR N-PSDB; AAX80968.  
XX  
PT Inhibiting activity of T cells against target cells useful for treating  
XX  
PS autoimmune diseases and allergy.  
XX  
PS Claim 9; Fig 1B; 79pp; English.  
XX  
The invention describes a method for inhibiting activity of T lymphocytes against a target cell by treating the cell with a soluble form of a CD8 molecule. The method is used as immunosuppressive therapy, e.g. in patients undergoing transplantation, but also for treating autoimmune diseases and allergy, e.g. exacerbation of asthma caused by viral infection. The CD8 protein inhibits cytotoxic T cells in vitro or in vivo, amnd its inhibitory activity can be adjusted by mutation. Treatment with CD8 protein provides more selective immunosuppression than use of corticosteroids. The present sequence represents the expressed fragment of human CD8 alpha protein

SQ Sequence 121 AA;
Query Match 100.0%; Score 642; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.3e-63;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQFRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSQNKPKA 60
Db 1 MSQFRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSQNKPKA 60
QY 61 AEGIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTT 120
Db 61 AEGIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTT 120
QY 121 P 121
Db 121 P 121

RESULT 2
ADS92792
ID ADS92792 standard; protein; 198 AA.
XX
AC ADS92792;
XX 16-DEC-2004 (first entry)
DT
XX A secreted CD8 alpha-chain protein alternative transcript.
DE
XX Immune response; cell-specific antigen; alloantigen; CD8;
KW CD8 alpha-chain; cellular immune response; humoral immune response;
KM transplant allograft; graft-versus-host disease; transplant.
XX Homo sapiens.
OS
XX WO2004083244-A2.
PN
XX 30-SEP-2004.
PD
XX 19-MAR-2004; 2004WO-US008574.
PF
XX 19-MAR-2003; 2003US-0456378P.
PR
XX (ISOG-) ISOGENIS INC.
PA
XX Qi Y, Zhang X, Konigsberg PJ;
PI
XX WPI; 2004-691022/67.
DR N-PSDB; ADS92793.
XX
PT Specifically inhibiting host immune responses to alloantigens, useful for
PT e.g. treating graft-versus-host disease, comprises contacting a target
PT cell expressing the antigen with an expression vector encoding a CD8
PT polypeptide.
XX
PS Disclosure; Fig 1; 98pp; English.
XX
CC The specification describes a method for specifically inhibiting a host
CC immune response to target cell-specific antigens (e.g. alloantigens). The
CC method comprises contacting a target cell expressing the antigen with an
CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
CC chain, where the CD8 polypeptide is expressed by the target cell and
CC where the host immune response against the target cell is specifically
CC inhibited. The method of the invention is useful for specifically
CC inhibiting both cellular and humoral immune responses to alloantigens,
CC thus finding use in extending the survival of transplant allografts and
CC in treating graft-versus-host disease in transplant recipients. The
CC present sequence represents an alternative transcript of a secreted alpha
CC -chain of a CD8 protein. This CD8 alpha-chain may be used in the method
CC of the invention.
XX
SQ Sequence 198 AA;

Query Match 99.2%; Score 637; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQFRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSQNKPKAA 61
Db 22 SQFRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSQNKPKAA 81
QY 62 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTT 121
Db 82 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTT 141

RESULT 3
ADS19438
ID ADS19438 standard; protein; 198 AA.
XX
AC ADS19438;
XX 16-DEC-2004 (first entry)
DT
XX Human secreted protein related to the CD8 alpha chain protein.
DE
XX human; gene therapy; CD8 alpha chain; cellular immune response;
KW humoral immune response; immunosuppressive.
XX Homo sapiens.
OS
XX WO2004083404-A2.
PN
XX 30-SEP-2004.
PD
XX 19-MAR-2004; 2004WO-US008567.
PF
XX 19-MAR-2003; 2003US-0456378P.
PR
XX (ISOG-) ISOGENIS INC.
PA
XX Qi Y, Zhang X, Konigsberg PJ;
PI
XX WPI; 2004-691049/67.
DR N-PSDB; ADS19439.
XX
PT New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
PT operably linked to a nucleic acid encoding a transmembrane polypeptide,
PT useful for inhibiting cellular and humoral components of the host immune
PT responses.
XX
PS Disclosure; Fig 1; 94pp; English.
XX
CC This invention relates to novel gene therapy vectors with reduced
CC immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
CC alpha chain operably linked to nucleic acid encoding a transmembrane
CC polypeptide and a second nucleic acid representing the therapeutic gene
CC of interest (for example ornithine carbamoyl transferase or beta
CC glucosidase), whereby transcriptional and translational control elements
CC direct expression thereof. The present invention describes a method to
CC reduce an immune response against antigens derived from a gene therapy
CC delivery system i.e. improving the expression of a therapeutic transgene
CC in a host and improving viral expression vectors with reduced
CC immunogenicity. Accordingly, these compositions are useful for inhibiting
CC both the cellular and humoral components of the host immune responses
CC against expression vectors and target cells transfected with the vectors.
CC As such, they exhibit immunosuppressive activity. This polypeptide is a
CC human secreted protein related to the CD8 alpha chain protein of the
CC invention.
XX
SQ Sequence 198 AA;
Query Match 99.2%; Score 637; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSONKPKAA 61  
Db 22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSONKPKAA 81  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 4  
ADZ26404  
ID ADZ26404 standard; protein; 198 AA.  
XX  
AC ADZ26404;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human CD8.  
XX  
KM cell culture; stem cell; CD8.  
XX  
OS Homo sapiens.  
XX  
PN WO2005030999-A1.  
XX  
PD 07-APR-2005.  
XX  
PF 24-SEP-2004; 2004WO-US031524.  
XX  
PR 25-SEP-2003; 2003US-0506221P.  
XX  
PR 08-OCT-2003; 2003US-0509594P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Ritz J, Wu CJ;  
XX  
DR WPI; 2005-273394/28.  
XX  
DR N-PSDB; ADZ26403.  
XX  
XX

PT Detecting lineage-specific cells in a biological sample, useful for  
PT determining the clinical outcome of a progenitor cell transfer in a  
PT subject, comprises identifying lineage-specific mRNA in the sample.  
XX  
PS Disclosure; SEQ ID NO 30; 393pp; English.  
XX  
XX

CC The invention relates to a method of detecting lineage-specific cells in  
CC a biological sample which comprises identifying lineage-specific mRNA in  
CC the sample. The methods are useful for determining the clinical outcome  
CC of a progenitor cell transfer in a subject, and for identifying or  
CC quantifying lineage-specific cells. The present sequence represents the  
CC amino acid sequence of a human protein used to identify lineage-specific  
CC cells.  
XX  
XX

SQ Sequence 198 AA;

Query Match 99.2%; Score 637; DB 9; Length 198;  
Best Local Similarity 100.0%; Pred. No. 9e-63;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSONKPKAA 61  
Db 22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSONKPKAA 81  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 5  
AAR49550  
ID AAR49550 standard; protein; 235 AA.  
XX  
AC AAR49550;  
XX

XX 25-MAR-2003 (revised)  
DT 20-AUG-1994 (first entry)  
XX  
XX Sequence of human CD8.  
DB  
XX gp39; T-cell antigen; CD40 ligand; B-cell proliferation; CD8;  
KM fusion protein; CD8; fusion protein.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP585943-A2.  
PN  
XX  
PD 09-MAR-1994.  
XX  
XX  
XX 03-SEP-1993; 93EP-00114153.  
PF  
XX  
XX 04-SEP-1992; 92US-00940605.  
PR  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA  
XX  
XX Aruffo A, Hollenbaugh D, Ledbetter JA;  
PI  
XX  
XX WPI; 1994-076264/10.  
DR  
XX  
XX N-PSDB; AAQ57986.  
DR  
XX

PT New nucleic acid encoding human gp39 T cell antigen - which is a ligand  
PT for the CD40 receptor, causing proliferation and differentiation of B  
PT cells and some cancer cells.  
XX  
XX  
XX Disclosure; Fig 9; 39pp; English.  
XX  
XX

CC The complete nucleic acid sequence of human gp39 (hgp39) protein  
CC (corresp. to cDNA) and the complete AA sequence of hgp39 are presented in  
CC AAQ57984 and AAR49548 respectively and contd. in plasmid CDM8-hgp39,  
CC deposited with the ATCC as E. coli, CDM8 MC1061/p3-hgp39 and assigned  
CC accession No. 69050. The human T cell antigen gp39 is a ligand for the  
CC CD40 receptor. Soluble gp39 may be produced using the expression vector  
CC CD8-gp39. Chimeric genes may be constructed by fusing sequences encoding  
CC the extracellular domains of gp39 and CD8, pref. murine or human CD8  
CC protein. Plasmid p3-shgp39 encoding the fusion protein of the  
CC extracellular domains from gp39 and CD8 is deposited in E.coli as ATCC  
CC 69049. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX

SQ Sequence 235 AA;

Query Match 99.2%; Score 637; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSONKPKAA 61  
Db 22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLYLSONKPKAA 81  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 6  
AAV21688  
ID AAV21688 standard; protein; 235 AA.  
XX  
AC AAV21688;  
XX  
DT 18-AUG-1999 (first entry)  
XX  
XX Human CD8 alpha protein.  
DE  
XX  
XX T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;  
KM autoimmune disease; allergy; asthma; viral infection; cytotoxic;  
KM corticosteroid; human; CD8 alpha protein.  
XX

OS	Homo sapiens.
XX	
PN	WO9921576-A1.
XX	
PD	06-MAY-1999.
XX	
PF	28-OCT-1998; 98WO-GB003235.
XX	
PR	28-OCT-1997; 97GB-00022779.
XX	
PA	(ISIS-) ISIS INNOVATION LTD.
XX	
PI	Jakobsen BK, Gao GF, Gerth UC, Sewell AK;
XX	
DR	WPI; 1999-385058/32.
DR	N-PSDB; AAX80967.
XX	
PT	Inhibiting activity of T cells against target cells useful for treating
PT	autoimmune diseases and allergy.
XX	
PS	Disclosure; Fig 1A; 79pp; English.
XX	
CC	The invention describes a method for inhibiting activity of T lymphocytes
CC	against a target cell by treating the cell with a soluble form of a CD8
CC	molecule. The method is used as immunosuppressive therapy, e.g. in
CC	patients undergoing transplantation, but also for treating autoimmune
CC	diseases and allergy, e.g. exacerbation of asthma caused by viral
CC	infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
CC	vivo, amnd its inhibitory activity can be adjusted by mutation. Treatment
CC	with CD8 protein provides more selective immunosuppression than use of
CC	corticosteroids. The present sequence represents a human CD8 alpha
CC	protein
XX	
XX	
SQ	Sequence 235 AA;
	Query Match 99.2%; Score 637; DB 2; Length 235;
	Best Local Similarity 100.0%; Pred. No. 1.1e-62;
	Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
DB	22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81
QY	62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121
DB	82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141
	RESULT 7
ABP54792	
ID	ABP54792 standard; protein; 235 AA.
XX	
AC	ABP54792;
XX	
DT	30-DEC-2002 (first entry)
XX	
DE	Human CD8.
XX	
KW	Chronic obstructive pulmonary disease; COPD; antagonist; CD8; human;
KW	transgenic animal; transgenic plant; antiasthmatic; antiinflammatory;
KW	antiarthritic; osteopathic; dermatological; immunosuppressive; cardiac;
KW	antiarteriosclerotic; hypotensive; antidiabetic; antibacterial; virucide;
KW	fungicide; parasiticide; cytostatic; nootropic; neuroprotective;
KW	antiparkinsonian; gene therapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	22..118
FT	/note= "epitope bound by COPD-related Ig-derived protein"
FT	119..235
FT	/note= "epitope bound by COPD-related Ig-derived protein"
XX	

PN	WO200272788-A2.
XX	
PD	19-SEP-2002.
XX	
PF	14-MAR-2002; 2002WO-US007946.
XX	
PR	14-MAR-2001; 2001US-0275652P.
XX	
PA	(GENZ ) CENTOCOR INC.
XX	
PI	Torphy T;
XX	
DR	WPI; 2002-740810/80.
XX	
PT	New isolated chronic obstructive pulmonary disease (COPD) related
PT	immunoglobulin derived protein or variant, useful for treating COPD-
PT	related conditions such as emphysema, asthma, chronic bronchitis or
PT	airflow obstruction.
XX	
XX	
PS	Claim 2; Page 108-109; 126pp; English.
XX	
CC	The present sequence is that of human CD8, an example of a chronic
CC	obstructive pulmonary disease (COPD)-related protein. The invention
CC	relates to novel COPD-related immunoglobulin (Ig)-derived proteins (see
CC	ABP54799-803) comprising at least one Ig complementarily determining
CC	region or at least one ligand binding region that specifically binds to
CC	at least one COPD-related protein, e.g. binding at least 1-3 amino acids,
CC	to the entire sequence, of amino acids 22-118 and 119-235 of the present
CC	sequence. The human COPD-related Ig-derived proteins act as antagonists
CC	to the COPD-related proteins. The invention provides the COPD-related Ig-
CC	derived proteins or specified portions or variants of them, nucleic acids
CC	encoding these polypeptides, vectors, host cells, transgenic animals and
CC	transgenic plants, and methods of making the COPD-related Ig-derived
CC	proteins, including therapeutic compositions. The proteins, nucleic
CC	acids, formulations and compositions are useful for treating COPD-related
CC	conditions such as COPD, emphysema, asthma, chronic bronchitis or airflow
CC	obstruction (claimed). They are also useful for treating or modulating
CC	COPD associated immune related diseases (arthritis, osteoarthritis,
CC	allergic rhinitis, lupus), cardiovascular diseases (congestive heart
CC	failure, arteriosclerosis, hypertension, angina pectoris), infections
CC	(bacterial, viral, fungal, parasitic), malignant diseases (cancer,
CC	leukaemia, Hodgkin's disease) and/or neurological diseases (Huntington's
CC	disease, Parkinson's disease, multiple sclerosis)
XX	
SQ	Sequence 235 AA;
	Query Match 99.2%; Score 637; DB 5; Length 235;
	Best Local Similarity 100.0%; Pred. No. 1.1e-62;
	Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 61
DB	22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAA 81
QY	62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121
DB	82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141
	RESULT 8
AAO19807	
ID	AAO19807 standard; protein; 235 AA.
XX	
AC	AAO19807;
XX	
DT	11-AUG-2003 (first entry)
XX	
DE	Human CD8alpha chain protein.
XX	
KW	Human; CD8alpha; MHC binding; mutant; mutein; immunosuppressive;
KW	antiallergic; cytotoxic T cell response; inhibitor.
XX	
OS	Homo sapiens.



XX WO2002102852-A2.  
PN  
XX  
PD 27-DEC-2002.  
XX  
PF 14-JUN-2002; 2002WO-GB002743.  
XX  
PR 14-JUN-2001; 2001GB-00014533.  
XX  
PA (AVID-) AVIDEX LTD.  
XX  
PI Jakobsen BK, Glick M;  
XX  
DR WPI; 2003-167488/16.  
DR N-PSDB; ABZ69260.  
XX  
XX  
PT New modified CD8 molecule having enhanced binding to major  
PT histocompatibility complex, and having a Serine53 of at least one CD  
PT alpha chain is mutated to another amino acid, useful for treating e.g.  
PT graft rejection or hypersensitivity.  
PS  
XX Disclosure; Fig 1A; 60pp; English.  
XX  
CC The present invention provides modified human CD8 molecules whose binding  
CC to major histocompatibility complex (MHC) is enhanced compared to wild  
CC type CD8. The modified CD8 molecule or a corresponding nucleic acid is  
CC useful in medicine, particularly in manufacturing a medicament for  
CC modulating CD8+ T cell response. The modified CD8 proteins and nucleic  
CC acids encoding such proteins are useful in immunosuppressive therapy,  
CC particularly as inhibitors of cytotoxic T cell responses, and for  
CC treating autoimmune disorders, hypersensitivity (e.g. allergic reaction),  
CC graft versus host disease, or graft rejection. The present sequence is a  
CC CD8 protein  
XX  
SQ Sequence 235 AA;  
  
Query Match 99.2%; Score 637; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SQFRVSPDLDRWTNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSONKPKAA 61  
Db 22 SQFRVSPDLDRWTNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSONKPKAA 81  
  
Qy 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIMYFSHPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIMYFSHPVFLPAKPTTTP 141  
  
RESULT 9  
ADD25613  
ID ADD25613 standard; protein; 235 AA.  
XX  
AC ADD25613;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Binding domain-immunoglobulin fusion protein-associated protein #84.  
XX  
KW Binding domain; immunoglobulin; fusion protein; cytosolic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IgG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX  
OS Unidentified.  
XX  
PN US2003118592-A1.  
XX  
PD 26-JUN-2003.

XX PF 25-JUL-2002; 2002US-00207655.  
XX  
XX 17-JAN-2001; 2001US-0367358P.  
PR 17-JAN-2002; 2002US-00053530.  
PR 03-JUN-2002; 2002US-0385691P.  
XX  
XX (GENE-) GENE-CRAFT INC.  
XX  
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
XX  
DR WPI; 2003-801317/75.  
XX  
PT New binding domain-immunoglobulin fusion protein, useful for treating a  
PT subject having or suspected of having a malignant condition or a B-cell  
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
XX  
XX  
PS Disclosure; SEQ ID NO 174; 157pp; English.  
XX  
CC The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an  
CC antigen. Also included are an isolated polynucleotide encoding the  
CC binding domain-immunoglobulin fusion protein, a recombinant expression  
CC construct comprising the polynucleotide (operably linked to a promoter),  
CC a host cell transformed or transfected with a recombinant expression  
CC construct, producing the binding domain-immunoglobulin fusion protein, a  
CC pharmaceutical composition comprising the binding domain-immunoglobulin  
CC fusion protein or polynucleotide and a carrier, and treating a subject  
CC having or suspected of having a malignant condition or a B-cell disorder.  
CC The binding domain-immunoglobulin fusion protein is useful for treating a  
CC subject having or suspected of having a malignant condition or a B-cell  
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
CC sclerosis or autoimmune disease. The present sequence is a binding domain  
CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
CC sequence data for this patent formed part of the printed specification  
CC and is also available in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not  
CC identified the sequences in the printed specification by their SEQ ID  
CC number therefore none of the sequences can be explicitly identified.  
XX  
SQ Sequence 235 AA;  
  
Query Match 99.2%; Score 637; DB 7; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SQFRVSPDLDRWTNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSONKPKAA 61  
Db 22 SQFRVSPDLDRWTNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLSONKPKAA 81  
  
Qy 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIMYFSHPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIMYFSHPVFLPAKPTTTP 141



```

RESULT 10
ADP12470
ID ADP12470 standard; protein; 235 AA.
XX
AC ADP12470;
XX
DT 12-AUG-2004 (first entry)
XX
DE Protein encoded by mRNA of the invention #80.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2479; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
SQ Sequence 235 AA;
XX
Query Match 99.2%; Score 637; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQFRVSPLDRTWNLGETVELKQVLLSNPTSGCSWLFQPRGAASPFLYLISQNKPKAA 61
DB 22 SQFRVSPLDRTWNLGETVELKQVLLSNPTSGCSWLFQPRGAASPFLYLISQNKPKAA 81
QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPEFLPAKPTTTP 121
DB 82 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYFFCSALSNSIMYFSHFVPEFLPAKPTTTP 141
XX
RESULT 11
ADQ18425
ID ADQ18425 standard; protein; 235 AA.
XX

```

AC	ADQ18425,
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	Human soft tissue sarcoma-upregulated protein - SEQ ID 1244.
XX	
KM	soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2004048938-A2.
XX	
PD	10-JUN-2004.
XX	
PF	26-NOV-2003; 2003WO-US038193.
XX	
PR	26-NOV-2002; 2002US-0429739P.
XX	
PA	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Aziz N, Ginsburg WM, Zlotnick A;
XX	
DR	WPI, 2004-441208/41.
XX	
PT	Early detection of soft tissue sarcoma comprises determining expression
PT	of a gene in a first soft tissue sample and a normal soft tissue sample
PT	and comparing the gene expression, also useful in treating soft tissue
PT	sarcoma.
PS	
XX	Example 2; SEQ ID NO 1244; 210pp; English.
XX	
CC	The invention relates to a novel method for detecting soft tissue sarcoma
CC	which comprises obtaining a first soft tissue sample from an individual
CC	and a normal soft tissue sample from the same or different individual,
CC	determining the expression of a gene in both samples and comparing the
CC	expression of the gene in both soft tissue samples, where a higher level
CC	of protein expression in the first soft tissue sample indicates the
CC	presence of soft tissue sarcoma. The method of the invention has
CC	cytostatic applications and may be useful for detecting soft tissue
CC	sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC	acid sequences may be useful in diagnostic and screening applications.
CC	The current sequence is that of a human soft tissue sarcoma-upregulated
CC	protein of the invention. The current sequence is not shown within the
CC	specification per se but was submitted in CD format by the inventor.
XX	
SQ	Sequence 235 AA;
	Query Match                      99.2%; Score 637; DB 8; Length 235;
	Best Local Similarity    100.0%; Pred. No. 1.1e-62;
	Matches 120; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
QY	
	2 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFGPGAAASPTFLLYLSQNKPKXA 61
DB	22 SQFRVSPDLRTWNLGETVELKCOVLLSNPTSGCSWLFGPGAAASPTFLLYLSQNKPKXA 81
QY	62 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPVFLPAKPTTTP 121
DB	82 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPVFLPAKPTTTP 141
RESULT 12	
ID	ADS92816
ID	ADS92816 standard; protein; 235 AA.
XX	
AC	ADS92816;
XX	
DT	16-DEC-2004 (first entry)
XX	
DE	Amino acid sequence of a CD8 alpha-chain protein.
XX	
KM	immune response; cell-specific antigen; alloantigen; CD8;
KM	CD8 alpha-chain; cellular immune response; humoral immune response;
KM	transplant allograft; graft-versus-host disease; transplant.

```

XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FH Peptide 1..21
XX FT /note= "signal peptide"
XX FT Domain 183..210
XX FT /note = transmembrane domain
XX PN WO2004083244-A2.
XX XX
XX PD 30-SEP-2004.
XX XX
XX PF 19-MAR-2004; 2004WO-US008574.
XX XX
XX PR 19-MAR-2003; 2003US-0456378P.
XX XX
XX PA (ISOG-) ISOGENIS INC.
XX XX
XX PI Qi Y, Zhang X, Konigsberg PJ;
XX XX
XX DR WPI; 2004-691022/67.
XX DR N-PSDB; ADS92817.
XX XX
XX PT Specifically inhibiting host immune responses to alloantigens, useful for
XX PT e.g. treating graft-versus-host disease, comprises contacting a target
XX PT cell expressing the antigen with an expression vector encoding a CD8
XX PT polypeptide.
XX XX
XX PS Disclosure; Fig 1; 98pp; English.
XX XX
XX CC The specification describes a method for specifically inhibiting a host
XX CC immune response to target cell-specific antigens (e.g. alloantigens). The
XX CC method comprises contacting a target cell expressing the antigen with an
XX CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
XX CC chain, where the CD8 polypeptide is expressed by the target cell and
XX CC where the host immune response against the target cell is specifically
XX CC inhibited. The method of the invention is useful for specifically
XX CC inhibiting both cellular and humoral immune responses to alloantigens,
XX CC thus finding use in extending the survival of transplant allografts and
XX CC in treating graft-versus-host disease in transplant recipients. The
XX CC present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha
XX CC -chain may be used in the method of the invention.
XX XX
XX SQ Sequence 235 AA;

Query Match 99.2%; Score 637; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61
DB 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 13
ADS92790
ID ADS92790 standard; protein; 235 AA.
XX XX
XX AC ADS92790;
XX XX
XX DT 16-DEC-2004 (first entry)
XX XX
XX DS Amino acid sequence of a CD8 alpha-chain protein.
XX XX
XX KW immune response; cell-specific antigen; alloantigen; CD8;
XX KW CD8 alpha-chain; cellular immune response; humoral immune response;
XX KW transplant allograft; graft-versus-host disease; transplant.
XX XX
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```

OS OS Homo sapiens.
XX XX
XX PN WO2004083244-A2.
XX XX
XX PD 30-SEP-2004.
XX XX
XX PF 19-MAR-2004; 2004WO-US008574.
XX XX
XX PR 19-MAR-2003; 2003US-0456378P.
XX XX
XX PA (ISOG-) ISOGENIS INC.
XX XX
XX PI Qi Y, Zhang X, Konigsberg PJ;
XX XX
XX DR WPI; 2004-691022/67.
XX DR N-PSDB; ADS92791.
XX XX
XX PT Specifically inhibiting host immune responses to alloantigens, useful for
XX PT e.g. treating graft-versus-host disease, comprises contacting a target
XX PT cell expressing the antigen with an expression vector encoding a CD8
XX PT polypeptide.
XX XX
XX PS Disclosure; Fig 1; 98pp; English.
XX XX
XX CC The specification describes a method for specifically inhibiting a host
XX CC immune response to target cell-specific antigens (e.g. alloantigens). The
XX CC method comprises contacting a target cell expressing the antigen with an
XX CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
XX CC chain, where the CD8 polypeptide is expressed by the target cell and
XX CC where the host immune response against the target cell is specifically
XX CC inhibited. The method of the invention is useful for specifically
XX CC inhibiting both cellular and humoral immune responses to alloantigens,
XX CC thus finding use in extending the survival of transplant allografts and
XX CC in treating graft-versus-host disease in transplant recipients. The
XX CC present sequence represents the alpha-chain of a CD8 protein. This CD8
XX CC alpha-chain may be used in the method of the invention.
XX XX
XX SQ Sequence 235 AA;

Query Match 99.2%; Score 637; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61
DB 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 81

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

RESULT 14
ADS19436
ID ADS19436 standard; protein; 235 AA.
XX XX
XX AC ADS19436;
XX XX
XX DT 16-DEC-2004 (first entry)
XX XX
XX DS Human CD8 alpha chain protein.
XX XX
XX KW gene therapy; CD8 alpha chain; cellular immune response;
XX KW humoral immune response; immunosuppressive.
XX XX
XX OS Homo sapiens.
XX OS
XX PN WO2004083404-A2.
XX XX
XX PD 30-SEP-2004.
XX XX
XX PF 19-MAR-2004; 2004WO-US008567.
XX XX
```

PR 19-MAR-2003; 2003US-0456378P.  
XX  
PA (ISOG-) ISOGENIS INC.  
XX  
PI Qi Y, Zhang X, Konigsberg PJ;  
XX  
DR WPI; 2004-691049/67.  
XX N-PSDB; ADS19437, ADS19462.  
XX  
PT New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain  
PT operably linked to a nucleic acid encoding a transmembrane polypeptide,  
PT useful for inhibiting cellular and humoral components of the host immune  
PT responses.  
XX  
PS Disclosure; Fig 1; 94pp; English.  
XX  
CC This invention relates to novel gene therapy vectors with reduced  
CC immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8  
CC alpha chain operably linked to nucleic acid encoding a transmembrane  
CC polypeptide and a second nucleic acid representing the therapeutic gene  
CC of interest (for example ornithine carbamoyl transferase or beta  
CC glucosidase), whereby transcriptional and translational control elements  
CC direct expression thereof. The present invention describes a method to  
CC reduce an immune response against antigens derived from a gene therapy  
CC in a host and improving viral expression vectors with reduced  
CC immunogenicity. Accordingly, these compositions are useful for inhibiting  
CC both the cellular and humoral components of the host immune responses  
CC against expression vectors and target cells transfected with the vectors.  
CC As such, they exhibit immunosuppressive activity. This polypeptide is the  
CC human CD8 alpha chain protein of the invention.  
XX  
SQ Sequence 235 AA;  
  
Query Match 99.2%; Score 637; DB 8; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61  
Db 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 81  
  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141  
  
RESULT 15  
ADZ26402  
ID ADZ26402 standard; protein; 235 AA.  
XX  
AC ADZ26402;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human CD8.  
XX  
KW cell culture; stem cell; CD8.  
XX  
OS Homo sapiens.  
XX  
PN WO2005030999-A1.  
XX  
PD 07-APR-2005.  
XX  
PF 24-SEP-2004; 2004WO-US031524.  
XX  
PR 25-SEP-2003; 2003US-0506221P.  
PR 08-OCT-2003; 2003US-0509594P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Ritz J, Wu CJ;

XX  
DR WPI; 2005-273394/28.  
DR N-PSDB; ADZ26401.  
XX  
PT Detecting lineage-specific cells in a biological sample, useful for  
PT determining the clinical outcome of a progenitor cell transfer in a  
PT subject, comprises identifying lineage-specific mRNA in the sample.  
XX  
PS Disclosure; SEQ ID NO 28; 393pp; English.  
XX  
CC The invention relates to a method of detecting lineage-specific cells in  
CC a biological sample which comprises identifying lineage-specific mRNA in  
CC the sample. The methods are useful for determining the clinical outcome  
CC of a progenitor cell transfer in a subject, and for identifying or  
CC quantifying lineage-specific cells. The present sequence represents the  
CC amino acid sequence of a human protein used to identify lineage-specific  
CC cells.  
XX  
SQ Sequence 235 AA;  
  
Query Match 99.2%; Score 637; DB 9; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61  
Db 22 SQFRVSPLDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 81  
  
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 121  
Db 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTTP 141

Search completed: April 5, 2006, 15:54:11  
Job time : 82 secs